



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 125803**

**TO: Bridget Bunner**  
**Location: REM/4C65/4C70**  
**Art Unit: 1647**  
**Wednesday, June 30, 2004**

**Case Serial Number: 10/069034**

**From: Deirdre Arnold**  
**Location: Biotech-Chem Library**  
**REM 1A64**  
**Phone: 571-272-2532**

**Deirdre.Arnold@uspto.gov**

### **Search Notes**

Thank you for using STIC services.

STIC-Biotech/ChemLib

105803

From: Bunner, Bridget  
Sent: Monday, June 28, 2004 3:24 PM  
To: STIC-Biotech/ChemLib  
Subject: sequence search

Hi! I'd like request a sequence search for case 10/069,034:

1. the amino acid sequence of SEQ ID NO: 28
2. the nucleic acid sequence of SEQ ID NO: 65

Thanks!

Bridget Bunner

Art Unit 1647  
Rem 4C65  
(571) 272-0881  
mailbox 4C70

Searcher: Arnold  
Phone: 3-2532  
Location: \_\_\_\_\_  
Date Picked Up: 6/29/04  
Date Completed: 6/30/04  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: 1  
AA Sequences: 1  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 29, 2004, 10:57:45 ; Search time 22 Seconds  
(without alignments)  
1074.759 Million cell updates/sec

Title: US-10-069-034-28

Perfect score: 2265  
Sequence: 1 MAWASRLGILLALLPWGA.....PEIFVYGVWISSGLFYQS 458

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/prodata/2/iaa/5a COMB.pap.\*  
2: /cgn2\_6/prodata/2/iaa/5a COMB.pap.\*  
3: /cgn2\_6/prodata/2/iaa/6a COMB.pap.\*  
4: /cgn2\_6/prodata/2/iaa/6a COMB.pap.\*  
5: /cgn2\_6/prodata/2/iaa/6a COMB.pap.\*  
6: /cgn2\_6/prodata/2/iaa/6a COMB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	286	12.6	487	3	US-08-431-517F-4
2	283	12.5	487	1	US-08-030-644-2
3	283	12.5	487	1	US-08-013-831-2
4	283	12.5	487	1	US-08-072-063-2
5	283	12.5	487	1	US-08-212-132-2
6	283	12.5	487	1	US-08-414-924-2
7	283	12.5	487	1	US-08-311-611A-69
8	283	12.5	487	1	US-08-311-611A-146
9	283	12.5	487	1	US-08-173-968-2
10	283	12.5	487	1	US-08-232-527-2
11	283	12.5	487	1	US-08-372-783-69
12	283	12.5	487	1	US-08-372-783-146
13	283	12.5	487	1	US-08-372-105-69
14	283	12.5	487	1	US-08-372-105-146
15	283	12.5	487	1	US-08-415-158-2
16	283	12.5	487	1	US-08-064-693-2
17	283	12.5	487	1	US-08-391-112-2
18	283	12.5	487	1	US-08-306-473A-69
19	283	12.5	487	1	US-08-306-473A-146
20	283	12.5	487	1	US-08-430-417-2
21	283	12.5	487	1	US-08-557-287-2
22	283	12.5	487	1	US-08-470-366-2
23	283	12.5	487	1	US-08-261-660A-12
24	283	12.5	487	1	US-08-209-762-69
25	283	12.5	487	1	US-08-644-290-2
26	283	12.5	487	1	US-08-378-228-2
27	283	12.5	487	1	US-08-927-438-2

28	283	12.5	487	1	US-08-473-344-69	Sequence 69, Appl
29	283	12.5	487	1	US-08-274-303-2	Sequence 2, Appl
30	283	12.5	487	1	US-07-915-720D-13	Sequence 13, Appl
31	283	12.5	487	1	US-08-435-855-2	Sequence 2, Appl
32	283	12.5	487	2	US-08-466-822-2	Sequence 2, Appl
33	283	12.5	487	2	US-08-466-824-2	Sequence 2, Appl
34	283	12.5	487	2	US-08-621-803-265	Sequence 265, App
35	283	12.5	487	2	US-08-466-826-2	Sequence 2, Appl
36	283	12.5	487	2	US-08-704-504-2	Sequence 2, Appl
37	283	12.5	487	2	US-08-485-445A-69	Sequence 69, Appl
38	283	12.5	487	2	US-08-485-445A-146	Sequence 146, App
39	283	12.5	487	2	US-08-621-259A-252	Sequence 252, App
40	283	12.5	487	2	US-08-586-133-2	Sequence 2, Appl
41	283	12.5	487	2	US-09-063-465-2	Sequence 2, Appl
42	283	12.5	487	2	US-08-862-785A-2	Sequence 2, Appl
43	283	12.5	487	2	US-09-081-166-2	Sequence 2, Appl
44	283	12.5	487	2	US-09-203-159-2	Sequence 2, Appl
45	283	12.5	487	3	US-09-099-725-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1  
US-08-431-517F-4  
; Sequence 4, Application US/08431517F  
; Patent No. 6265187  
; GENERAL INFORMATION:  
; APPLICANT: Scott, Randal W  
; APPLICANT: Marra, Marian N  
; TITLE OF INVENTION: RECOMBINANT ENDOTOXIN-NEUTRALIZING PROTEINS  
; FILE REFERENCE: 1103/113070US01  
; CURRENT APPLICATION NUMBER: US/08/431,517F  
; CURRENT FILING DATE: 1995-05-01  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 487  
; TYPE: PRT  
; ORGANISM: human  
; OTHER INFORMATION: BPI cDNA and amito acid sequence (Figure 3)  
US-08-431-517F-4

Query Match 12.6%; Score 286; DB 3; Length 487;  
Best Local Similarity 22.4%; Pred. No. 3.2e-21;  
Matches 109; Conservative 104; Mismatches 229; Indels 44; Gaps 17;

QY	3	WASRLGILLALLPVVGASTPTGVVRLNKAALSYVSEIGKAPLORAL-QVTVPHFLD---	58
DB	15	WWS-LMWLVAIGTAVTAANVNGVVRISQKGLDYASQQTALQKELKRIKIDYDSFK	73
QY	59	-----WSGEALQPTIRILNVH---VPRHLKF-IAGFGVRLAAANFTFKVFAPE	106
DB	74	IKHLGKHGHSFYSDMIREFQLPSSQISVFNVLGKFSISNANIKISGKWAQKRFKMSG	133
QY	107	PLELTLP-VELLADTRV-TQSSIRTPVVISACLSGSHANEFGDGNSTSHA--LLVLVQ	162
DB	134	NFDLSIEGMSIGADLKLSNPTSGKPTITCSSC---SSHINSVHVHISKVGWLIQLFH	190
QY	163	KHITKAVLSNKL-----CLISNLVQG-VNVHLGTLGLNVPGPSQIRYSVMVPTVTSDY	217
DB	191	KKIESALRNKMSQVCEKVTNSVSSKLOQYFQTLPTWTKIDSVAGINYGIVAPNTAET	250
QY	218	ISLEVNALFLGKPIILPTDATPFVLP--RHVGTGSMATVGLSQQLFDSALLLQKAG	275
DB	251	LDVQMKGEFYSENH-----HNPPFPAPWMEFAAHDWVYGLSDYFFNTAGLVQKAG	305
QY	276	ALNLDITGQI--RSDNLTNTSALGLIIEVARQPEPMPVVLKVLGATPVAMLHTNNA	333
DB	306	VLMKTLRDMIPKESKRLTTPFGGFLPEVAKKFN--MKIQIHVSASTPPLHSVQPT	362
QY	334	TLRLQPFVEV--LATASNAFQSLFSLGVVNLRLQLSVSKVKLQGTTSVLGDVQVLTVAS	391

Db 363 GLTFYPAVDVQALAVLPNSLSASLFLIGHHTTGSMEVSAESNRLVGELK-LDRLLLELKH 421  
 QY 392 SNVGFDLDDQVRLMGTVPEKPLDLHLNALLAMGIALPGVNLHYVAPFIFFVEGVVVIS 451  
 Db 422 SNIGFPFVELLQDIMNYIVPILVPRVNEKLOKGPPLTPPARVQVLYNWNVYLQPHQNLFLFG 481  
 QY 452 SGLFYQ 457  
 Db 482 ADVYK 487

RESULT 2  
 US-08-030-644-2  
 ; Sequence 2, Application US/08030644  
 ; Patent No. 5348942  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Little, Roger G. II  
 ; APPLICANT: Gazzano-Santoro, Helene  
 ; APPLICANT: Parent, James Brian  
 ; TITLE OF INVENTION: Therapeutic uses of  
 ; Bactericidal/Permeability-Increasing Protein Products  
 ; NUMBER OF SEQUENCES: 2  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: USA  
 ; ZIP: 60606-6402  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/030,644  
 ; FILING DATE: 19930312  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Sharp, Jeffrey S.  
 ; REGISTRATION NUMBER: 31,879  
 ; REFERENCE/DOCKET NUMBER: 31229  
 ; TELEPHONE: 312/474-6300  
 ; TELEFAX: 312/474-0448  
 ; TELEX: 25-3856  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 487 amino acids  
 ; TYPE: AMINO ACID  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-030-644-2

Query Match 12.5%; Score 283; DB 1; Length 487;  
 Best Local Similarity 22.4%; Pred. No. 6.5e-21;  
 Matches 109; Conservative 104; Mismatches 229; Indels 44; Gaps 17;

QY 3 WASRLGLMALLLPYVGASTGTVVRLNKAALSYVSEIGKAELOAL-QVTVPHELD--- 58  
 Db 15 WVS-LMVLVAGTAVTAANVGVVRIISQKGLDYASQQGTAALQKELKRIKIPDYSDSFK 73  
 QY 59 -----WSGALQFTRIRILNVH---VPRHLXP-IAGFGVRLAAANFTFKVRAPE 106  
 Db 74 IKHLCKGHYFYSMDIRFQLPSSQISMPVNYGLAFESINAIKISGKWKAKRFLKWSG 133  
 QY 107 PLELTLP-VELLADTRV-TQSSIRTPVVISACS-LFSGHANEFDCGNSNTHA--LLVLVQ 162  
 Db 134 NFDLSIEGMSISADLKLGSNPTSGKPTITCSC---SSHINSVHVHISKVKVGLIQLFH 190  
 QY 163 KHIAVLNKL-----CLISNLVQG-VNVLGTL-LGLNPVGESQIRYSMSVPTVTSY 217  
 Db 191 KRIESALRNKMSQVCEKVTNSVSSKLQYFQTLFVMTKIDSVAGINVLVAPPATTAT 250

QY 218 ISLEVNVLFLGKPIILLPTDATPVLIP--RHVGTGSMATVCLSQOLESALLLQKAG 275  
 Db 251 LDVQMGKEFYSNH-----HNPPFPAPPVWMEPPAHDHVMVILGSLDYFFNTAGLVYQEAG 305  
 QY 276 ALNLDTIGOL--RSDNLIINTSALGRLEPEVARQPEPPMFVVLKVRIGATPPVAMLHTNNA 333  
 Db 306 VLKMTLRDDMIPKESKRLTTTKFFGTFLPEVAKKFPN--MKIQIHVSASTPPLSVQPT 362  
 QY 334 TLRLOPFVEVLATA--SNSAFOSLSLDVVMNRLQLSVSKVLQTTTSVLGDVQVLTVAS 391  
 Db 363 GLTFYPAVDVQAFVLPNSLSASLFLIGHHTTGSMEVSAESNRLVGELK-LDRLLLELKH 421  
 QY 392 SNVGFDLDDQVRLMGTVPEKPLDLHLNALLAMGIALPGVNLHYVAPFIFFVEGVVVIS 451  
 Db 422 SNIGFPFVELLQDIMNYIVPILVPRVNEKLOKGPPLTPPARVQVLYNWNVYLQPHQNLFLFG 481  
 QY 452 SGLFYQ 457  
 Db 482 ADVYK 487

RESULT 3  
 US-08-013-801-2  
 ; Sequence 2, Application US/08013801  
 ; Patent No. 5420019  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Theofan, Georgia  
 ; APPLICANT: Horwitz, Arnold  
 ; APPLICANT: Burke, David  
 ; APPLICANT: Baltaian, Manik  
 ; APPLICANT: Grinna, Lynn S  
 ; TITLE OF INVENTION: Stable Bactericidal/Permeability-  
 ; Increasing Protein Products and Pharmaceutical  
 ; Compositions Containing the Same  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
 ; ADDRESSEE: Bicknell  
 ; STREET: Two First National Plaza  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: USA  
 ; ZIP: 60603  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/013,801  
 ; FILING DATE: 02 FEB 1993  
 ; CLASSIFICATION: 424  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Meyers, Thomas C.  
 ; REGISTRATION NUMBER: P-36,989  
 ; REFERENCE/DOCKET NUMBER: 27129/30911  
 ; TELEPHONE: 312/346-5750  
 ; TELEFAX: 312/346-9740  
 ; TELEX: 25-3856  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 487 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-013-801-2

Query Match 12.5%; Score 283; DB 1; Length 487;  
 Best Local Similarity 22.4%; Pred. No. 6.5e-21;  
 Matches 109; Conservative 104; Mismatches 229; Indels 44; Gaps 17;



QY 3 WASRLGLLLALLLPVVGASTRGTVVRLNKAALSYVSEIGKAPLQAL-QVTVPHFLD--- 58  
Db 15 WVS-LMWLVAIGTAVTAAPVGVVRIKSGLDYASQQGTAALQKELRIKIPDYSDSK 73  
QY 59 -----WSGEALQPTRIRILNVH---VPRHLKF-IAGFGVRLAAANFTFKVRAPE 106  
Db 74 IKHLKGHSYFYSMDIREFQLPSSQISVVPVGLKFSINANIKISGKWKAKRFLKMSG 133  
QY 107 PLELTLP-VELLADTRV-TQSSIRTPVVISACSLFSGHANEFDSNSTSHA--LLVLVQ 162  
Db 134 NFDLSIEGMSISADLKGSNPTSGKPTTTCSSC---SSHINSVHVHISKSKVGLIQLPH 190  
QY 163 KHIAVLNKL-----CLISINLQVQ-VNVHLGTLGLNPVGPESQIRYSMSVPTVTSY 217  
Db 191 KKIESALRNKMSQVCEKVTNSVSKLQPYFQTLPMVKIDSVAGINYLVAAPPATTAT 250  
QY 218 ISLEVNALFLLGKPIILPTDATPVLP--RHVGTGSMATVGLSQQLFDGALLLQKAG 275  
Db 251 LDVQKGEFYSENH-----HNPPFPAPVMEPPAAHDMVILGLSDYFNTAGLVYQEG 305  
QY 276 ALNLDITQQL--RSDNLLNTSALGRLLPEVARQPEPMPVVLKVLGATPVAMLHTNNA 333  
Db 306 VLKMTLRDDMPKSKERLTTFKFTFLPEVAKKPK---MKIQHVASASTPPHLSVQPT 362  
QY 334 TRLQPFVEVLATA--SNSAFQSLFSLDVVNLRLQLSVSKVKGTLTSVLGDVQLTVAS 391  
Db 363 GLTFYPAVDVQAFVLPNSSLASFLICGHTTGSMEVSAESNRLVGELK-LDRLLLELKH 421  
QY 392 SNVGFIDTQVRLTGMVTFEXPLDLHALLANGIALPGVNLHVVAPEIFVYEGYVVIS 451  
Db 422 SNIGFPFVELLDIMNYIVPIVLPRVNEKLGKFPPLTPARVQLVNVVLQPHQNFLFG 481  
QY 452 SGLFYQ 457  
Db 482 ADVVYK 487

## RESULT 4

US-08-072-063-2  
; Sequence 2, Application US/08072063  
; Patent No. 5447913  
; GENERAL INFORMATION:  
; APPLICANT: Theofan, Georgia  
; APPLICANT: Grinna, Lynn S  
; APPLICANT: Horwitz, Arnold  
; TITLE OF INVENTION: BPI-Immunoglobulin Fusion Proteins  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/072,063  
; FILING DATE: 19930519  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meyers Thomas C.  
; REGISTRATION NUMBER: 36,989  
; REFERENCE/DOCKET NUMBER: 30659  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:

; LENGTH: 487 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-072-063-2  
Query Match 12.5%; Score 283; DB 1; Length 487;  
Best Local Similarity 22.4%; Pred. No. 6.5e-21;  
Matches 109; Conservative 104; Mismatches 229; Indels 44; Gaps 17;  
QY 3 WASRLGLLLALLLPVVGASTRGTVVRLNKAALSYVSEIGKAPLQAL-QVTVPHFLD--- 58  
Db 15 WVS-LMWLVAIGTAVTAAPVGVVRIKSGLDYASQQGTAALQKELRIKIPDYSDSK 73  
QY 59 -----WSGEALQPTRIRILNVH---VPRHLKF-IAGFGVRLAAANFTFKVRAPE 106  
Db 74 IKHLKGHSYFYSMDIREFQLPSSQISVVPVGLKFSINANIKISGKWKAKRFLKMSG 133  
QY 107 PLELTLP-VELLADTRV-TQSSIRTPVVISACSLFSGHANEFDSNSTSHA--LLVLVQ 162  
Db 134 NFDLSIEGMSISADLKGSNPTSGKPTTTCSSC---SSHINSVHVHISKSKVGLIQLPH 190  
QY 163 KHIAVLNKL-----CLISINLQVQ-VNVHLGTLGLNPVGPESQIRYSMSVPTVTSY 217  
Db 191 KKIESALRNKMSQVCEKVTNSVSKLQPYFQTLPMVKIDSVAGINYLVAAPPATTAT 250  
QY 218 ISLEVNALFLLGKPIILPTDATPVLP--RHVGTGSMATVGLSQQLFDGALLLQKAG 275  
Db 251 LDVQKGEFYSENH-----HNPPFPAPVMEPPAAHDMVILGLSDYFNTAGLVYQEG 305  
QY 276 ALNLDITQQL--RSDNLLNTSALGRLLPEVARQPEPMPVVLKVLGATPVAMLHTNNA 333  
Db 306 VLKMTLRDDMPKSKERLTTFKFTFLPEVAKKPK---MKIQHVASASTPPHLSVQPT 362  
QY 334 TRLQPFVEVLATA--SNSAFQSLFSLDVVNLRLQLSVSKVKGTLTSVLGDVQLTVAS 391  
Db 363 GLTFYPAVDVQAFVLPNSSLASFLICGHTTGSMEVSAESNRLVGELK-LDRLLLELKH 421  
QY 392 SNVGFIDTQVRLTGMVTFEXPLDLHALLANGIALPGVNLHVVAPEIFVYEGYVVIS 451  
Db 422 SNIGFPFVELLDIMNYIVPIVLPRVNEKLGKFPPLTPARVQLVNVVLQPHQNFLFG 481  
QY 452 SGLFYQ 457  
Db 482 ADVVYK 487  
RESULT 5  
US-08-212-132-2  
; Sequence 2, Application US/08212132  
; Patent No. 5447913  
; GENERAL INFORMATION:  
; APPLICANT: Little, Roger G.  
; APPLICANT: Ammons, William Steve  
; TITLE OF INVENTION: Therapeutic Uses of Bactericidal/Permeability-  
; TITLE OF INVENTION: Increasing Protein Dimer Products  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/212,132  
; FILING DATE:  
; CLASSIFICATION: 514

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Jeffrey S.
; REGISTRATION NUMBER: 31,879
; REFERENCE/DOCKET NUMBER: 27129/32297
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-212-132-2

Query Match 12.5%; Score 283; DB 1; Length 487;
Best Local Similarity 22.4%; Pred. No. 6.5e-21;
Matches 109; Conservative 104; Mismatches 229; Indels 44; Gaps 17;

QY 3 WASRLGLLALLPVVGASTPGTVRLNKAALSYVEIGKAPLQAL-QVTVPHELD--- 58
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
15 WVS-LMWLVAGTAVTAANVPGVVRISQKGLDYASQOQTAALQKELKIKIPDYSEFK 73
QY 59 -----WSGALQPTRIRILNVH---VPRHLKF-IAGFVRLLAANFTFKVRAPE 106
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
74 IXHLKGHYFSYMDIREFQPSQISVMVNLKFSISNANIKISGKWKAKRFLKMSG 133
QY 107 PLELTLP-VELLADTRV-TQSSIRTPVWSISACSLFSGHANEFDGNSNSTSHA--LLVLVQ 162
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
134 NFDLSIEGMSISADLKLSNPTSGKPTITCSCS---SSHINSVHVHISKSKVGLLQLFH 190
QY 163 KHIAVLSNKL-----CLISINLVQGVNVLHTLGLNVPVGSQIRYSMVSVPTVTSY 217
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
191 KKIESALRNKMSQVCEKVTNSVSKLQFYFTLPVMTKIDSVAGINYLGLVAPPATTAT 250
QY 218 ISLEYNVFLILGKPIILLPTDTPFVLP--RHVGTEGSMATVGLSQQLFDSALLLQKAG 275
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
251 LDVQMKGFYSENH-----HNPPFPAPVMEFPAADRMYVGLSDYFFNTAGLVQEGAG 305
QY 276 ALNLDITQL--RSDNLLNTSALGRLEPEVARQPEPMPVVLKVLGATPVAMLHTNNA 333
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
306 VLKMTLRDDMIPKESKFRLLTKFFGFLPEVAKKFPN---MKIQIHVSASTPPHLSVQPT 362
QY 334 TLRLQPFVEVLATA--SNSAFQSLFSLDVMNLRQLSVSKVQLQGTTSVLGDVQVLTAS 391
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
363 GLTFPVDVQAFVLPNSLSLASFLIGXHTTGSMESVSAESNRLVGELK-LDRLLLELKH 421
QY 392 SNVGFIDTQVRLTGMGTVEKPEPLLDHNLALLAMGIALPGVNLHYVAPFIFFVGVVWIS 451
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
422 SNIGFFPVELLDQIMNYIPIVLPRVNEKLGKGFPLTPPARVOLYNVVLQPHQNFLLFG 481
QY 452 SGLFYQ 457
Db 482 ADVVYK 487

```

## RESULT 6

```

US-08-414-924-2
; Sequence 2, Application US/08414924
; Patent No. 5494896
; GENERAL INFORMATION:
; APPLICANT: Hansbrough, John F.
; TITLE OF INVENTION: Method of Treating Conditions
; TITLE OF INVENTION: Associated With Burn Injuries
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America

```

```

; ZIP: 60606-6432
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,924
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Jeffrey S.
; REGISTRATION NUMBER: 31,879
; REFERENCE/DOCKET NUMBER: 27129/32297
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-414-924-2

```

```

Query Match 12.5%; Score 283; DB 1; Length 487;
Best Local Similarity 22.4%; Pred. No. 6.5e-21;
Matches 109; Conservative 104; Mismatches 229; Indels 44; Gaps 17;

QY 3 WASRLGLLALLPVVGASTPGTVRLNKAALSYVEIGKAPLQAL-QVTVPHELD--- 58
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
15 WVS-LMWLVAGTAVTAANVPGVVRISQKGLDYASQOQTAALQKELKIKIPDYSEFK 73
QY 59 -----WSGALQPTRIRILNVH---VPRHLKF-IAGFVRLLAANFTFKVRAPE 106
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
74 IXHLKGHYFSYMDIREFQPSQISVMVNLKFSISNANIKISGKWKAKRFLKMSG 133
QY 107 PLELTLP-VELLADTRV-TQSSIRTPVWSISACSLFSGHANEFDGNSNSTSHA--LLVLVQ 162
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
134 NFDLSIEGMSISADLKLSNPTSGKPTITCSCS---SSHINSVHVHISKSKVGLLQLFH 190
QY 163 KHIAVLSNKL-----CLISINLVQGVNVLHTLGLNVPVGSQIRYSMVSVPTVTSY 217
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
191 KKIESALRNKMSQVCEKVTNSVSKLQFYFTLPVMTKIDSVAGINYLGLVAPPATTAT 250
QY 218 ISLEYNVFLILGKPIILLPTDTPFVLP--RHVGTEGSMATVGLSQQLFDSALLLQKAG 275
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
251 LDVQMKGFYSENH-----HNPPFPAPVMEFPAADRMYVGLSDYFFNTAGLVQEGAG 305
QY 276 ALNLDITQL--RSDNLLNTSALGRLEPEVARQPEPMPVVLKVLGATPVAMLHTNNA 333
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
306 VLKMTLRDDMIPKESKFRLLTKFFGFLPEVAKKFPN---MKIQIHVSASTPPHLSVQPT 362
QY 334 TLRLQPFVEVLATA--SNSAFQSLFSLDVMNLRQLSVSKVQLQGTTSVLGDVQVLTAS 391
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
363 GLTFPVDVQAFVLPNSLSLASFLIGXHTTGSMESVSAESNRLVGELK-LDRLLLELKH 421
QY 392 SNVGFIDTQVRLTGMGTVEKPEPLLDHNLALLAMGIALPGVNLHYVAPFIFFVGVVWIS 451
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
422 SNIGFFPVELLDQIMNYIPIVLPRVNEKLGKGFPLTPPARVOLYNVVLQPHQNFLLFG 481
QY 452 SGLFYQ 457
Db 482 ADVVYK 487

```

## RESULT 7

```

US-08-311-611A-69
; Sequence 69, Application US/08311611A
; Patent No. 5523288
; GENERAL INFORMATION:
; APPLICANT: Cohen, Jonathan

```

```

; APPLICANT: Kung, Ada H.C.
; APPLICANT: Lambert, Jr., Lewis H.
; TITLE OF INVENTION: Method for Treating Gram-Negative Bacterial
; TITLE OF INVENTION: Infection by Administration of
; TITLE OF INVENTION: Bactericidal/Permeability-Increasing
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311.611A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/273,401
; FILING DATE: 11-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/125,651
; FILING DATE: 22-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Jeffrey S.
; REGISTRATION NUMBER: 31,879
; REFERENCE/DOCKET NUMBER: 32251
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: "rBPI"
US-08-311-611A-69

Query Match 12.5%; Score 283; DB 1; Length 487;
Best Local Similarity 22.4%; Pred. No. 6.5e-21;
Matches 109; Conservative 104; Mismatches 229; Indels 44; Gaps 17;

QY 3 WASRLGLLALLLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQAL-QVTVPHFLD--- 58
Db 15 WVS-LMWLVAGTAVTAANPGVVRISQKGLDYASQQGTAALQKELKRIKIPYDSDFK 73
QY 59 -----MSGEALQPTRILNVH---VRLHKE-IGAGFVRLAAANFTKVRAP 106
Db 74 IKHLGKHGHSFYSDMTDEEQLPSPQISWPNVGLKFSINANTKISGKWKAKRFLKMSG 133
QY 107 PLELTLP-VELLADTRV-TQSSIRTPVWSISACLSFGSHANEPDGSNSTSHA--LLVLVQ 162
Db 134 NFDLSIEGMSISADLLKLSGNSPTSGKPTICSSC---SSHINSVHVHLSKVKGNLLQLFH 190
QY 163 KHKAVLSNKL-----CLISNLVQG-VNVLHGLTGLNPNVGPESQTRYSMVSVPTVTSY 217
Db 191 KKIESALRNKMSQVCEKVTNSVSSKLQFYFTPLPMTKIDSVAGINYLGAAPPATTART 250
QY 218 ISLEVNVLFLGKPIILPTDTPFVLP--RVVGTGSMATVCLSQOLFDSALLILQKAG 275
Db 251 LDVQKGEFYSNH-----HNPPFPAPPVMEPPAAHDMVVLGLSDYFFNTAGLVQVEAG 305
QY 276 ALNLDITGOL--RSDNLTNSALGRLLPEVARQFPPEPMPVVLKVRIGATPVAMLHTNNA 333

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Db 306 VLKMTLRDDWIPKESKRLTKFFGTFLEPAVKFPN---MKIQIHVSASTPEHLSVQPT 362
QY 334 TLRLQPFVEVLATA--SNSAFQSLPSLDVVVNRLQLSVSKVKLGTTSTVLGVDQLTFAS 391
Db 363 GUTFPADVQAFVLPNSLASLFLIGHMTTGSMEVSAESNELVGLK-LDRLLLELKH 421
QY 392 SNVGFIDTDQVRLTMGTVEKPLDHLNALLAMGIALPGVNLHYVAPEIFVVEGYVVIS 451
Db 422 SNIGFPFVELLODKNYIVPILVLRVNEKLGKGPPLTPARVOLNNVWVQPHQNFLEFG 481
QY 452 SGLFYQ 457
Db 482 ADWVYK 487

```

## RESULT 8

```

US-08-311-611A-146
; Sequence 146, Application US/08311611A
; Patent No. 5523288
; GENERAL INFORMATION:
; APPLICANT: Cohen, Jonathan
; APPLICANT: Kung, Ada H.C.
; TITLE OF INVENTION: Method for Treating Gram-Negative Bacterial
; TITLE OF INVENTION: Infection by Administration of
; TITLE OF INVENTION: Bactericidal/Permeability-Increasing
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311.611A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/273,401
; FILING DATE: 11-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/125,651
; FILING DATE: 22-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Jeffrey S.
; REGISTRATION NUMBER: 31,879
; REFERENCE/DOCKET NUMBER: 32251
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 146:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-311-611A-146

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```

Query Match 12.5%; Score 283; DB 1; Length 487;
Best Local Similarity 22.4%; Pred. No. 6.5e-21;
Matches 109; Conservative 104; Mismatches 229; Indels 44; Gaps 17;

QY 3 WASRLGLLALLLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQAL-QVTVPHFLD--- 58
Db 15 WVS-LMWLVAGTAVTAANPGVVRISQKGLDYASQQGTAALQKELKRIKIPYDSDFK 73

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QY 59 -----WSGEALQPTRIRILNVH---VPRHLKPF-IAGFVRLLAANFTKVFRAPE 106
DQ 74 IKHLGKGYSFYMDIREFOLPSSQISWYVNGVKFSISNANIKISGKWKAKQKFLKMSG 133
QY 107 PLELTLP-VELLADTRV-TQSSIRTPVVSISACLSFGSHANEFDGNSNSTSHA--LLVLVQ 162
DQ 134 NFDLSIEGMSISADLKLGSNPTSGKPTITCSC---SSHINSVHVHISKSKVGWLIQLFH 190
QY 163 KHKAVLSNKL-----CLISNLVQGV-VNVHLGTLIGLNPVGPESQIRYSVMVSVPTVTSY 217
DQ 191 KKLIALRNKQNSQVCEKVTNSVSSKLPYQTLTPVMTKIDSVAGINGLVAPATTAAET 250
QY 218 ISLEVNVLFLGKPIILPTDTPFVLP--RHVGTGSMATVGLSQQLFDSALLLQKAG 275
DQ 251 LDVQMKGEFYSENH-----HNPPFPAPVMEFFAAHDMVVLGLSDYFFNTAGLVYQAG 305
QY 276 ALNLDTITQGL--RSDDNLNLTSALEGLIPEVAROPPEMPVWLKVRIGATPVAMLHTNNA 333
DQ 306 VLKMTLRDDMIPEKSKPRLTITKFFGTFLPEVAKFPN---MKIQIHVSASTPPHLSVQPT 362
QY 334 TLRQPPFVEVLATA--SNSAFQSLFSLDVVVNLRLQLSVSKVKLGTTSLVGLDVQLTVAS 391
DQ 363 GLTFYPAVDVQAFVLPNSLSIASLFLIGMHTTGSMEVSAESNRLVGLK-LDRLLLELKH 421
QY 392 SNVGFIDTQVRLTMGTVEKPLDLHNLALLANGIALPGVNLHVHVAPEIFVYEGYVVIS 451
DQ 422 SNIGFPFVELLDIMNYIVPILVPRVNEKLGKGFPLTPARVOLYNVVLQPHQNFLLFG 481
QY 452 SGLFYQ 457
DQ 482 ADVYIK 487

```

## RESULT 9

```

US-08-173-968-2
; Sequence 2, Application US/08173968
; Patent No. 5576292
; GENERAL INFORMATION:
; APPLICANT: Weiss, Peter
; APPLICANT: Weiss, Jerrold
; TITLE OF INVENTION: Biologically Active
; TITLE OF INVENTION: Bactericidal/Permeability-increasing Protein Fragments
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howard M. Frankfort
; STREET: 805 Third Ave.
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,968
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/754,204
; FILING DATE: 26-AUG-1991
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Frankfort, Howard M.
; REGISTRATION NUMBER: 32,613
; REFERENCE/DOCKET NUMBER: 5969/05982US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 527-7700
; TELEFAX: (212) 753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

```

```

; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: blood
; CELL TYPE: promyelocytic leukemia cells
; US-08-173-968-2

```

## Query Match 12.5%; Score 283; DB 1; Length 487;

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Best local Similarity 22.4%; Ered. No. 6.5e-21;
Matches 103; Conservative 104; Mismatches 229; Indels 44; Gaps 17;
QY 3 WASRGLLLALLLPVVGASTPGTVVRLNKAALSYSVEIGKAPLQAL-QVTVPFPLD--- 58
DQ 15 WVS-LMVVAIGTAVTAANVGVVVRISOKGLDVASQGTAAALQKELKRIKIPDYSDFK 73
QY 59 -----WSGEALQPTRIRILNVH---VPRHLKPF-IAGFVRLLAANFTKVFRAPE 106
DQ 74 IKHLGKGYSFYMDIREFOLPSSQISWYVNGVKFSISNANIKISGKWKAKQKFLKMSG 133
QY 107 PLELTLP-VELLADTRV-TQSSIRTPVVSISACLSFGSHANEFDGNSNSTSHA--LLVLVQ 162
DQ 134 NFDLSIEGMSISADLKLGSNPTSGKPTITCSC---SSHINSVHVHISKSKVGWLIQLFH 190
QY 163 KHKAVLSNKL-----CLISNLVQGV-VNVHLGTLIGLNPVGPESQIRYSVMVSVPTVTSY 217
DQ 191 KKLIALRNKQNSQVCEKVTNSVSSKLPYQTLTPVMTKIDSVAGINGLVAPATTAAET 250
QY 218 ISLEVNVLFLGKPIILPTDTPFVLP--RHVGTGSMATVGLSQQLFDSALLLQKAG 275
DQ 251 LDVQMKGEFYSENH-----HNPPFPAPVMEFFAAHDMVVLGLSDYFFNTAGLVYQAG 305
QY 276 ALNLDTITQGL--RSDDNLNLTSALEGLIPEVAROPPEMPVWLKVRIGATPVAMLHTNNA 333
DQ 306 VLKMTLRDDMIPEKSKPRLTITKFFGTFLPEVAKFPN---MKIQIHVSASTPPHLSVQPT 362
QY 334 TLRQPPFVEVLATA--SNSAFQSLFSLDVVVNLRLQLSVSKVKLGTTSLVGLDVQLTVAS 391
DQ 363 GLTFYPAVDVQAFVLPNSLSIASLFLIGMHTTGSMEVSAESNRLVGLK-LDRLLLELKH 421
QY 392 SNVGFIDTQVRLTMGTVEKPLDLHNLALLANGIALPGVNLHVHVAPEIFVYEGYVVIS 451
DQ 422 SNIGFPFVELLDIMNYIVPILVPRVNEKLGKGFPLTPARVOLYNVVLQPHQNFLLFG 481
QY 452 SGLFYQ 457
DQ 482 ADVYIK 487

```

## RESULT 10

```

US-08-232-527-2
; Sequence 2, Application US/08232527
; Patent No. 5578568
; GENERAL INFORMATION:
; APPLICANT: Ammons, William Steve et al.
; TITLE OF INVENTION: Method of Treating Conditions Associated with
; TITLE OF INVENTION: Intestinal Ischemia/Reperfusion
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/372,783
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/273,540
FILING DATE: 11-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,762
FILING DATE: 11-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/183,222
FILING DATE: 14-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Heier
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 27129/32415
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: "rBPI"
US-08-372-783-69

Query Match 12.5%; Score 283; DB 1; Length 488
Best Local Similarity 22.4%; Pred. No. 6.5e-21;
Matches 139; Conservative 104; Mismatches 229; Indels

Qy 3 WNRIGLLALLLPVVGASTFGVWRLNKAALSYVSEIGHKAPLQAL-
Db 15 WVS-LMVLVAIGTAVTAANNPGVWVRISQGLDYASQQGTAALQKELK
Qy 59 -----WSGEALQPTRIILNVH---VPLRLHKF-IAGFGVRLLA-
Db 74 IKHGKGHYFSMDIREFQSQISMVENVGLKFSISNANKIKSGK-
Qy 107 PLEITLP-VELLADTRY-TQSSIRTPVVSISACLSFGSHANEFDGNSNS-
Db 134 NFDLSIEGMSISADLKLGSNPTSGKPTITCSSC---SSHINSVHVHHS-
Qy 163 KHKAVLSNKL-----CLISNLVQG-VNVHLGTILGNLPVGPESQIRY-
Db 191 KTESALREKQNSQVCEKVTNSVSKLPQYFOTLPVMTKIDSVAGINY-
Qy 218 ISLEVNAVFLLGKPIILPTDAPVLP--RHVGTGSMATVGLSQOL-
Db 251 LDVMQGEFYSNH-----HNPPFPAPPMEFPAADRVYVLGSLDYF-
Qy 276 ALNADITGOL--RSDNMLNTSALGRILPEVARQFPEPFWVLKVLIG-
Db 306 VLKMTLDDMIPIKESKRLTIKFGITLPEVAKKFPN---MKIQIHVS-
Qy 334 TLRLQPPVEVLATA--SNSAFQSFLSDVVNLRQLSVSKVKLGKTT-

```

363 GLTFYPAVDVQAFVLPNSLSIASFLICMHTTGSMEVSAESNRILVGBELK-LDRLLLELKH 421  
392 SNVGFIDTQVRLMGTVFEKFLDLHALLAMGIALPGVNLHYVAPEIFVYGVVIS 451  
422 SNIGFFVLLQDIMNVIVPILVPRVNEKLOKGFPLTPARVQLYNNVLIQPHQNFLLFG 481  
452 SGLFYQ 457  
482 ADVYK 487

RESULT 12  
US-08-372-783-146  
Sequence 146, Application US/08372783  
Patent No. 5578572  
GENERAL INFORMATION:  
APPLICANT: Horwitz, Arnold H.  
APPLICANT: Lambert, Lewis H.  
TITLE OF INVENTION: Anti-Gram-Positive Bacterial Methods and  
TITLE OF INVENTION: Materials  
NUMBER OF SEQUENCES: 237  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/372,783  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/273,540  
FILING DATE: 11-JUL-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/209,762  
FILING DATE: 11-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/183,222  
FILING DATE: 14-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Rin-Laures, Li-Hsien  
REGISTRATION NUMBER: 33,547  
REFERENCE/DOCKET NUMBER: 27129/32415  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ. ID NO. 146:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 487 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-372-783-146

Query Match 12.5%; Score 283; DB 1; Length 487;  
Best Local Similarity 22.4%; Pred. No. 6.5e-21;  
Matches 183; Conservative 104; Mismatches 229; Indels 44; Gaps 17;

3 WASRLGLLALLPVVVGASTPGTVRLNKAALSVSEIGKAPLORAL-QTVVPHFLD--- 58  
15 WWS-LMWLVAGTAVTAANPVGVVVRISQGLDYASQQGTAALQKELKRIKIPYSDSFX 73  
59 -----NSGEALQPTRILNVH---VPLRLKF-IAGFGVRLLAANFTKVFRAPE 106  
74 IKILGKHYSFYSDIREFOLPSSQISMVNVGLKFSISNANIKISKWKAQRFLKMSG 133

QY 107 PLELTLP-VELLADTRV-TQSSIRTPVVISIACSLSFSGHANEFDSGNSNSTSHA--LLVLVQ 162  
DB 134 NFDLSIGMSISADLKIGSNFTSKPTITCSC---SSHINSVHVHISKSKVGMILQLPH 190  
QY 163 KHIKAVLSNKL---CLISINLVQ--VNVHLGTILGNPVGPEQIRYSVMYVPTVTSY 217  
DB 191 KXIESALRNKMSQVCEKVTNSVSKLPYFTLPVMTKIDSVAGINYLVAPEATTAE 250  
QY 218 ISLEVNVLFLGKPIILPTDTPVLP--RHVTEGSMATVGLSQQLPDSALLLQKAG 275  
DB 251 LDVQMGFEYSNH-----HNPPFPAPVMEFFAAHDMVYLGLSDYFNTAGLVYQAG 305  
QY 276 ALNLDITQQL--RSDDNLLNTSALGRILPEVAROFPEPMPVVLKVRIGATPVAMLHTNNA 333  
DB 306 VLKWLIRDDMIPKESKFLTKFPFTLPEVAKFPN---MKIQHVSASTPPLHSVQPT 362  
QY 334 TLRLOPFVVIATA--SNSAFQSLFSLDVMVNLRLQLSVSKVLOGTTSVLGDVOLTVAS 391  
DB 363 GLTFYPAVDVQAFVLPNSLSIASFLICMHTTGSMEVSAESNRILVGBELK-LDRLLLELKH 421  
QY 392 SNVGFIDTQVRLMGTVFEKFLDLHALLAMGIALPGVNLHYVAPEIFVYGVVIS 451  
DB 422 SNIGFFVLLQDIMNVIVPILVPRVNEKLOKGFPLTPARVQLYNNVLIQPHQNFLLFG 481  
QY 452 SGLFYQ 457  
DB 482 ADVYK 487

RESULT 13  
US-08-372-105-69  
Sequence 69, Application US/08372105  
Patent No. 5627153  
GENERAL INFORMATION:  
APPLICANT: Little, Roger G.  
APPLICANT: Lim, Edward  
APPLICANT: Lambert, Lewis H.  
APPLICANT: Scannon, Patrick J.  
TITLE OF INVENTION: Anti-Fungal Materials and Methods  
NUMBER OF SEQUENCES: 227  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/372,105  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/273,540  
FILING DATE: 11-JUL-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/209,762  
FILING DATE: 11-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/183,222  
FILING DATE: 14-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Rin-Laures, Li-Hsien  
REGISTRATION NUMBER: 33,547  
REFERENCE/DOCKET NUMBER: 27129/32415  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 69:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 487 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FEATURE:  
 NAME/KEY: misc feature  
 OTHER INFORMATION: "BPI"  
 US-08-372-105-69

Query Match 12.5%; Score 283; DB 1; Length 487;  
 Best Local Similarity 22.4%; Pred. No. 6.5e-21;  
 Matches 109; Conservative 104; Mismatches 229; Indels 44; Gaps 17;

QY 3 WASRLGLLALLLPVVGASTGTVVRLNKAALSYVSEIGKAPLORAL-QVTVPHLD--- 58  
 DB 15 WVS-LMWLVAGTAVTAANVPGVVRISQKGLDYASQQTAALQKELKRIKIPDYSDSEFK 73

QY 59 -----WSGEALQPTRIRILNVH---VPRHLKF-IAGFGVRLAAANFTFKVRAPE 106  
 DB 74 IKHLGKHYSFYSDIREFQLPSSQISWVNVGLKFSISNANIKISGKWKAKRFLKMSG 133

QY 107 PLELTLP-VELLADTRV-TQSSIRTPVVISACSLFSGHANFDSNSTSHA--LLVLVQ 162  
 DB 134 NFDLSIEGMS-SADIKLGSNPTSGKPTTICSSC---SSHINSVHVHISKSKVGLIQLF 190

QY 163 KHIAVLSNKL-----CLGISNLVQG-VNVLGLTGLNLPVGPESQIRYSMVSVPTVTSY 217  
 DB 191 KKIESALEKKNKNSQVCEKVTNSVSKLQIPYFOTLPWTKIDSVAGINYLGLVAPPATTAT 250

QY 218 ISLEVNVLFLGKPIILPTDAPFVLP--RHVGTGSMATVGLSQQLFDSALLLQKAG 275  
 DB 251 LDVQMKGEFYSENH-----HNPPFPAPVMEFPAADHDMVYGLSDYFENTAGLVYQV 305

QY 334 TLRLOPFVEVLATA--SNSAFOSFLSDVNVNRLQLSVSKVLOGTTSVLGSDVQITVAS 391  
 DB 363 GLTFYPAVDVQAFVLPNSSLASLELGHHTTGSMEVSAESNRLVGELEK-LDRILLELKH 421

QY 392 SNVGFIDTQVRLTGMGTVEKPELIDHLLNALLAMGIALPGVNLHYVAPEIFYEGYVVIS 451  
 DB 422 SNIGFPFVELLQDLMNYIVPILVLRVNEKLGKGFPLTPARVQLYNVVYLQEQNFLLFG 481

QY 452 SGLFYQ 457  
 DB 482 ADVYK 487

## RESULT 14

US-08-372-105-146

Sequence 146, Application US/08372105

Patent No. 5627153

GENERAL INFORMATION:

APPLICANT: Little, Roger G.

APPLICANT: Lim, Edward

APPLICANT: Lambert, Lewis H.

APPLICANT: Scannon, Patrick J.

TITLE OF INVENTION: Anti-Fungal Materials and Methods

NUMBER OF SEQUENCES: 227

CORRESPONDENCE ADDRESS:

ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/372,105

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/273,540

FILING DATE: 11-JUL-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/209,762

FILING DATE: 11-MAR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/183,222

FILING DATE: 14-JAN-1994

ATTORNEY/AGENT INFORMATION:

NAME: Ric-Laures, Li-Hsien

REGISTRATION NUMBER: 33,547

REFERENCE/DOCKET NUMBER: 27129/32415

TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 146:

SEQUENCE CHARACTERISTICS:

LENGTH: 487 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-372-105-146

Query Match 12.5%; Score 283; DB 1; Length 487;

Best Local Similarity 22.4%; Pred. No. 6.5e-21;

Matches 109; Conservative 104; Mismatches 229; Indels 44; Gaps 17;

QY 3 WASRLGLLALLLPVVGASTGTVVRLNKAALSYVSEIGKAPLORAL-QVTVPHLD--- 58

DB 15 WVS-LMWLVAGTAVTAANVPGVVRISQKGLDYASQQTAALQKELKRIKIPDYSDSEFK 73

QY 59 -----WSGEALQPTRIRILNVH---VPRHLKF-IAGFGVRLAAANFTFKVRAPE 106

DB 74 IKHLGKHYSFYSDIREFQLPSSQISWVNVGLKFSISNANIKISGKWKAKRFLKMSG 133

QY 107 PLELTLP-VELLADTRV-TQSSIRTPVVISACSLFSGHANFDSNSTSHA--LLVLVQ 162

DB 134 NFDLSIEGMS-SADIKLGSNPTSGKPTTICSSC---SSHINSVHVHISKSKVGLIQLF 190

QY 163 KHIAVLSNKL-----CLGISNLVQG-VNVLGLTGLNLPVGPESQIRYSMVSVPTVTSY 217

DB 191 KKIESALEKKNKNSQVCEKVTNSVSKLQIPYFOTLPWTKIDSVAGINYLGLVAPPATTAT 250

QY 218 ISLEVNVLFLGKPIILPTDAPFVLP--RHVGTGSMATVGLSQQLFDSALLLQKAG 275

DB 251 LDVQMKGEFYSENH-----HNPPFPAPVMEFPAADHDMVYGLSDYFENTAGLVYQV 305

QY 276 ALNDITQL--RSDNLLNTSALGRILPEVARQPEPMPVVLKVRIGATPVAMLHTNNA 333

DB 306 VLKMTLRDDMTPKESKFLTTKFFGTFLPEVAKKPPN---MKIQIHVSASTPPHLSVQPT 362

QY 334 TLRLOPFVEVLATA--SNSAFOSFLSDVNVNRLQLSVSKVLOGTTSVLGSDVQITVAS 391

DB 363 GLTFYPAVDVQAFVLPNSSLASLELGHHTTGSMEVSAESNRLVGELEK-LDRILLELKH 421

QY 392 SNVGFIDTQVRLTGMGTVEKPELIDHLLNALLAMGIALPGVNLHYVAPEIFYEGYVVIS 451

DB 422 SNIGFPFVELLQDLMNYIVPILVLRVNEKLGKGFPLTPARVQLYNVVYLQEQNFLLFG 481

QY 452 SGLFYQ 457

DB 482 ADVYK 487

## RESULT 15

US-08-415-158-2

? Sequence 2, Application US/08415158  
? Patent No. 5639727  
? GENERAL INFORMATION:  
? APPLICANT: Little, Roger G. II  
? APPLICANT: Gazzano-Santoro, Helene  
? APPLICANT: Parent, James Brian  
? TITLE OF INVENTION: Therapeutic uses of  
? TITLE OF INVENTION: Bactericidal/Pertussis-Increasing Protein Products  
? NUMBER OF SEQUENCES: 2  
? CORRESPONDENCE ADDRESS:  
? ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
? STREET: 6300 Sears Tower, 233 South Wacker Drive  
? CITY: Chicago  
? STATE: Illinois  
? COUNTRY: USA  
? ZIP: 60606-6402  
? COMPUTER READABLE FORM:  
? MEDIUM TYPE: Floppy disk  
? COMPUTER: IBM PC compatible  
? OPERATING SYSTEM: PC-DOS/MS-DOS  
? SOFTWARE: Patent In Release #1.0, Version #1.25  
? CURRENT APPLICATION DATA:  
? APPLICATION NUMBER: US/08/415,158  
? FILING DATE:  
? CLASSIFICATION: 514  
? PRIOR APPLICATION DATA:  
? APPLICATION NUMBER: US/08/093,202  
? FILING DATE:  
? APPLICATION NUMBER: US 08/030,644  
? FILING DATE: 12-MAR-1993  
? ATTORNEY/AGENT INFORMATION:  
? NAME: Sharp, Jeffrey S.  
? REGISTRATION NUMBER: 31,879  
? REFERENCE/DOCKET NUMBER: 31580  
? TELECOMMUNICATION INFORMATION:  
? TELEPHONE: 312/474-6300  
? TELEFAX: 312/474-0448  
? TELEX: 25-3856  
? INFORMATION FOR SEQ ID NO: 2:  
? SEQUENCE CHARACTERISTICS:  
? LENGTH: 487 amino acids  
? TYPE: amino acid  
? TOPOLOGY: linear  
? MOLECULE TYPE: protein  
? US-08-415-158-2

Query Match 12.5%; Score 283; DB 1; Length 487;  
Best Local Similarity 22.4%; Pred. No. 6.5e-21;  
Matches 109; Conservative 104; Mismatches 229; Indels 44; Gaps 17;  
QY 3 WASRIGLALLLPVVGASTFTGVRLNKAALSYVSEIGKAPLQAL-QVTVPHFLD--- 58  
DB 15 WVS-LMWLVAGTAAVAVPGVVVRIQKGLDYASQQTAALQKELKRIKIPDYSDFK 73  
QY 59 -----WSEALQPTIRILNVH---VPRHLKF-IAGFGVRLAAANFTFKVFRAP 106  
DB 74 IKHLGKHYSYFMDIRFQPSQISMVVNVGLKFSISNANIKISGKWKAKQKFLKMSG 133  
QY 107 FLELTLP-VELLATRV-TQSSIRTPVVISACSLFSGHANEFDSNSTSHA--LLVLVQ 162  
DB 134 NFDLSIEGMSIADLKLGSNFTSGKPTTCSCC---SSHINSVHVHISKVGVLIQLFH 190  
QY 163 KHIKAVLSNKL-----CLISINLVQG-VNVHLGTLIGLNPVGESQIRYSMVSVPTVTSY 217  
DB 191 KKIESALRNKNSQVCEKVTNSVSKLQPYFOTLPVMTKIDSVAGINYLVPATTAT 250  
QY 218 ISLEVNAVLELLGKPIILPTDAPVLP--RHVGTGSMATVGLSQQLFDSNALLLQKAG 275  
DB 251 LDVQMKGEFYSNH-----HNPPFPAPVPMFPPAAHDMVYILGSDYFFNT-AGLVYQ 305  
QY 276 ALNLDITQGL--RSDNLTNSALGRLIPEVARQFPEPMPVVLKVLGATPVAMLHTNNA 333  
DB 306 VLKWLTRDDMPKESKRLTKFFCTELPEVAKFPPN---MKIQLHVSASTPPLSVQPT 362

QY 334 TLRLOPFVEVLATA--SNSAFQSLFSLDWVNVNRLQLSVSKVKLAQTTSVLGDVOLTVAS 391  
DB 363 GLTFYPAVDVQAFVLPNSSLASLFLIGMTTGSMEVSAESNRLVGLK-LDRLLLELKH 421  
QY 392 SNVGEIDTDQVRLTGMVTFEKLPLDLHNLALAMGIALPGVNLHVVAPEIFYEGYVVIS 451  
DB 422 SNIGFPVVELQDINMYIVPILVLPVNEKLQKGFPLETPARVQVLYNVVLPQHPHFLFG 481  
QY 452 SGLFYQ 457  
DB 482 ADVVYK 487

Search completed: June 29, 2004, 11:01:30  
Job time : 24 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 29, 2004, 10:56:44 ; Search time 21 Seconds  
(without alignments)  
2097.891 Million cell updates/sec

Title: US-10-069-034-28

Perfect score: 2265  
Sequence: - MAWASRLGLLALLLPWGA.....PEIFVVEGYVWISSGLFYQS 458

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78.\*

1: Fir1.\*

2: Fir2.\*

3: Pir3.\*

4: Pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	392.5	17.3	470	2 S17447	probable ligand-bi
2	353	15.6	473	2 S17448	probable ligand-bi
3	283	12.5	487	2 A30909	bactericidal/perme
4	256	11.3	481	2 A54136	lipopolysaccharide
5	251	11.1	482	2 B35843	lipopolysaccharide
6	247.5	10.9	482	2 S0180	bactericidal perme
7	246.5	10.9	481	2 I56246	lipopolysaccharide
8	241	10.6	477	2 A35843	lipopolysaccharide
9	173	7.6	493	2 I49370	plasma phospholipi
10	159.5	7.0	493	2 A53533	phospholipid trans
11	132	5.8	250	4 A43383	bactericidal/perme
12	132	5.8	576	2 T22700	hypothetical prote
13	120.5	5.3	488	2 C86183	hypothetical prote
14	116	5.1	606	2 T29190	hypothetical prote
15	113	5.0	974	2 A90140	conserved hypothet
16	112	4.9	554	2 T15438	hypothetical prote
17	111	4.9	493	2 A53176	cholesterol ester
18	109.5	4.8	1131	2 T41144	hypothetical serin
19	109.5	4.8	1749	2 S75071	hypothetical prote
20	109	4.8	4436	2 E71086	hypothetical prote
21	105.5	4.7	553	2 A81057	hypothetical integ
22	105	4.6	4152	2 T31102	filamentous hemagg
23	104	4.6	1455	2 F88941	protein R13D11.7 [
24	103.5	4.6	1176	2 T18042	ice nucleation pro
25	103	4.5	488	2 D64108	glucanate transpor
26	103	4.5	766	2 T07171	subtilisin-like pr
27	102.5	4.5	812	2 T39817	hypothetical prote
28	102.5	4.5	1118	1 SYBVC	carbamoyl-phosphat
29	102	4.5	637	2 A54000	sodium/phosphate c

## ALIGNMENTS

### RESULT 1

S17447

probable ligand-binding protein RY2G5 - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 13-Jan-1995 #sequence\_revision 22-May-1998 #text\_change 05-Nov-1999

C;Accession: S17447

R;Dear, T.N.; Boehm, T.; Keverne, E.B.; Rabbitts, T.H.

EMBO J. 10, 2813-2819, 1991

A;Title: Novel genes for potential ligand-binding proteins in subregions of the olfacto:

A;Reference number: S17447; MUID:92007724; PMID:1915264

A;Accession: S17447

A;Molecule type: mRNA

A;Residues: 1-470 <DEA>

A;Cross-references: EMBL:X60660; NID:g57731; PIDN:CAA43067.1; PID:g57732

A;Experimental source: Olfactory mucosa

C;Genetics:

A;Gene: RY2G5

C;Keywords: olfaction

Query Match 17.3%; Score 392.5; DB 2; Length 470;  
Best Local Similarity 26.9%; Pred. No. 66-22;  
Matches 109; Conservative 81; Mismatches 182; Indels 33; Gaps 5;

Qy	67	TRIRLNHVPRHLKFIAGGVRLAAANFTKVFRAPELELTLPVELADTRVTQSS	126
Db	80	TGLRIVELTLPVRSVRLPGGVLSLYTVAINGKS-IGFLDIAVEVNTAKVRLTMDR	139
Qy	127	IRTPVVSISACSLFSGH-----ANFDGSNSTSHALLVLQKHKAVLSNKLCLS	176
Db	140	TGYPRLVIERCDTLGIGIKVKLRGLLPNLDN-----LVNRLANVLPDLLCPI	189
Qy	177	ISNLVQGVNVHLGTLGLNPGVPESQIRYSMSVPTVTSDYISLEVNAY-----F	227
Db	190	VYVVLGVNDQLGLVDSVPLTGILGSVYTFSSPLVTGFELELDLNTINVEAGGDLIDY	249
Qy	228	ELGKPIILTDATPPVLPVRHVGTEGSMATVGLSQQLFDSALLLQKAGALNDITGQRS	287
Db	250	PLGRPAMLPQPELPPMGNDNTNSQLA---ISANFLSSVLTMLQKQALDIDITDGMFE	306
Qy	288	DNMLNTSALGRILPEVAQFPPEMPVLKVRIGATPVAMLHTNNATLRLOPFFVEVATA	347
Db	307	DLPLPLTSTLIGALPKVFOQYPSRELTIRIQPNPPTVTLQDKALKVKVFATSEVVWSQ	366
Qy	348	SNSAFOSLSLDVNVNLRQLSVSKVKLOGTTSVLGDVQLTVASSNVGFEIDTQVRLMG	407
Db	367	PNDVETTCILVDVTDLLASFSVEGDKLM-IDAKLQKTSUNRTSNVGNPFIENLWVE	425
Qy	408	TVFEKPELLDHLNALLAMGIALPGVNVNLHYVAPEIFVYEGVWISS	452
Db	426	KIFDLAFPMANAILGSGVLPKILNIDFSNADIDVLELLVLST	470

30	101.5	4.5	498	2	AD0854
31	101.5	4.5	637	2	S01509
32	101	4.5	487	2	T18952
33	101	4.5	523	2	T08854
34	100	4.4	1774	2	S13178
35	100	4.4	2406	2	A54148
36	100	4.4	2515	2	S47008
37	99.5	4.4	392	2	T04150
38	99	4.4	325	2	AF2665
39	99	4.4	333	2	E97447
40	99	4.4	430	2	G75408
41	99	4.4	898	2	B65236
42	99	4.4	998	2	C91281
43	99	4.4	898	2	D86132
44	98.5	4.3	409	2	H97889
45	98.5	4.3	707	2	JC7763

probable permease  
NADH2 dehydrogenas  
hypothetical prote  
dihydrolipoamide d  
6-methylsalicylic  
odz protein - frui  
tenascin-like prot  
RAD23 protein homo  
conserved hypothet  
hypothetical prote  
probable transport A  
Mg(2+) transport ATP  
Mg2+ transport ATP  
conserved hypothet  
neuronal leucine-r

## RESULT 2

S17448  
A:Status: nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-374, 'L', 376-487 <WIL>  
A:Experimental source: HL-60 cells  
A:Note: Sequence extracted from NCBI backbone (NCBI:P149855)  
R:Ooi, C.E.; Weiss, J.; Elsbach, P.; Frangione, B.; Mannion, B.  
J. Biol. Chem. 262, 14891-14894, 1987  
A:Title: A 25-kDa amino-terminal fragment carries all the antibacterial activities of  
A:Reference number: S17447; MUID:9207724; PMID:1915264  
A:Accession: S17448  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-473 <DEA>  
A:Cross-references: EMBL:X60658; NID:957733; PIDN:CAA43065.1; PID:957734

Query Match 15.6%; Score 353; DB 2; Length 473;  
Best Local Similarity 25.3%; Pred. No. 5.9e-19;  
Matches 12; Conservative 93; Mismatches 212; Indels 52; Gaps 12;

QY 9 LLLALLPVVG-ASTPGTVVRANKAALSYVSEIGKA-----FLORALQVTVPH--- 55  
DB 10 LLWGLATPCGLLETVGLARIK-----DELGKALQNSLVGCPILQNVLTGTVTSVNOG 63  
QY 56 -----FLWSG-----EALOPTIRILNVHVRPLHLKPTIAGFGVRLAAANFT 98  
DB 64 LLGAGLLGGGLSYGGLFSIWERLSGLKIELT--LPTVS-KLLPGVGVL---SLHT 118  
QY 99 FKVFRAPEP---LELTLPVELLADTRVTCSSIRTPVWSISACLSFGSHANEFGNSN 154  
DB 119 KVSLEHSGPLVGLQLAAEWNSSKVALGMSPRGTPIILKRCNTLGHISLTSGLLPT- 177  
QY 155 HALLVLVQHKAVLSNKLCLSLSNLVQGVNVHLGLTGLNVPGRSQIRYSMVSVPTVT 214  
DB 178 -PIFGLVEQTLCKLPGLCPVDSVLSVNVNELLGATLSIVZGLPLSGVEFTLALPLIS 236  
QY 215 SYVISEVNAVIL-FLGKPIILPTDTPVPLPHVGTSGMACVGLSQQLFDSALLLQK 273  
DB 237 NQYIELDINPIVKSIAAGVDIDPKPLPKMP---PKEDHTSQVTVPLVFNTPVGLLOT 293  
QY 274 AGALNLDITGQLRSDNLTNTSALGRILPEVARQFPEPMPVILKVLGATPVAMLTNNA 333  
DB 294 NGALDLITPEMVPNPIPIITDOLALAPALGKLPQGLLILSLKMSPIILLONKKV 353  
QY 334 TLRLQFVFLVATASNAFQSLFSLDVVNLRLQLSVSKVLQGTTSVLGDVOLTVAASN 393  
DB 354 TVSIPTVTHVLSVPOQTPVALLFQMGVMTLNALHVPSTTKLHISLS-LERLTVQLASSF 412  
QY 394 VGFITDQVRLMGTVFEXPLDLHINALLAMGIALPGVNLHVVAPEIFVYEGYVVIS 451  
DB 413 SQPFDSARLEEMLSDVVRAAYXQKLNHELVGIPKILNVNFANESVDVNIENAVLT 470

## RESULT 3

A30909  
A:Status: nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-487 <GRA>  
A:Cross-references: GB:J04739; NID:gl19528; PIDN:AAA51841.1; PID:gl19529  
R:Wildie, C.G.; Seilhamer, J.J.; McGrogan, M.; Ashton, N.; Snable, J.L.; Lane, J.C.; Leon  
J. Biol. Chem. 269, 17411-17416, 1994  
A:Title: Bactericidal/permeability-increasing protein and lipopolysaccharide (LPS)-bindi  
A:Reference number: A54136; MUID:94292492; PMID:7517398  
A:Accession: B54136

Query Match 12.5%; Score 283; DB 2; Length 487;  
Best Local Similarity 22.4%; Pred. No. 1.2e-13;  
Matches 109; Conservative 104; Mismatches 229; Indels 44; Gaps 17;  
QY 3 WASRLGLLALLPVVGASTPGTVVRANKAALSYVSEIGKAPLQAL-QVTVPHFLD--- 58  
DB 15 WVS-LMVLVAIGTAVTAANVPGVVVRISOKGLDYASQQGTRALQKELKRIKIDYSDSFX 73  
QY 59 -----WSGEALOPTIRILNVH---VPLHLKF-IAAGFVRLAAANFTFKVRAPE 106  
DB 74 IKHLGKHYSFYSDIREFQLPSSQISVSNVNLKFSISNANIKISGKNKAKRFLKMSG 133  
QY 107 PLELTLP-VELLADTRV-TQSSIRTPVWSISACLSFGSHANEFGNSNSTSHA--LLVLVQ 162  
DB 134 NFDLSIEGMSIADLKLGSNPTSGKPTITCSSC---SSHINSVHVHISKVGWLLQLFH 190  
QY 163 KHIAKVLNKL---CLSLSNLVQGVNVHLGLTGLNVPGRSQIRYSMVSVPTVTSY 217  
DB 191 KLESALRNKMSQVCEKVTNSVSKLQFYQTLPTWKIDSVAGINYLGVAPATTAET 253  
QY 218 ISLEVNAILFLGKPIILPTDTPVFLP--RHVGTSGMATVGLSQQLFDSALLLQKAG 275  
DB 251 LQVKGGEFYSENH-----HNPPFPAPVMEFPAADHVRVYLGLSYFFNTAGLVYQAG 305  
QY 276 ALNLDITGQL--RSDNLTNTSALGRILPEVARQFPEPMPVILKVLGATPVAMLTNNA 333  
DB 306 VLKMTLRDDMIKPKSKFRUTTKFFGTFLEVAKKFN---MKIQIHVSASTPPLHSVQPT 362  
QY 334 TLRLQFVFLVATA--SNSAFQSLFSLDVVNLRLQLSVSKVLQGTTSVLGDVOLTVA 391  
DB 363 GLTFFPAVDVQAFVLPNSLASLFLIGMTTGSMEVSAESNRLVGELK-LDLILLELKH 421

QY 392 SNVGFIDTQGRILMGTVFEPKPLDHLNALLAMGIALPGVNNLHYVAPEIFVYEGYVVIS 451  
Db 422 SNIGPEPVELLODMYVIVILVLRVNMELKQGFPLTPARVQLVNNVQLPQHNFLEFG 481  
QY 452 SGLFYQ 457  
Db 482 ADVYK 487

## RESULT 4

A54136  
lipopolysaccharide-binding protein - human  
N:Alternate names: LBP; LPS-binding protein  
C:Species: Homo sapiens (man)  
J:Exp. Med. 269, 1741-17416, 1994  
A:Title: Bactericidal/permeability-increasing protein and lipopolysaccharide (LPS)-binding protein  
A:Reference number: A54136; MUID:94292492; PMID:7517398  
A:Accession: A54136  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: nucleic acid  
A:Residues: 1-481 <WIL>  
A:Experimental source: liver  
A:Note: sequence extracted from NCBI backbone (NCBIP:149401)  
C:Superfamily: lipopolysaccharide-binding protein

Query Match 11.3%; Score 256; DB 2; Length 481;  
Best Local Similarity 23.9%; Pred. No. 1.3e-11;  
Matches 118; Conservative 94; Mismatches 210; Indels 72; Gaps 23;  
QY 9 LLLALL--PVGASTPTGVRLNKAALSYVSEIGKAPLQ-RALQVTPHFELDSGEAL 64  
Db 11 LLLALLTTPCALGANPGLVARIITDKGLQYAAQEGLLALQSELLRITLP---DFTGDLR 67  
QY 65 QP-----TRILNVH-VPRLL--LKFIAGFVRLAA-----ANFTKVPRAPEPLE- 109  
Db 58 IPHVGGRYEFHSLNIHSCHELLHSALRPVPGGGLSLISDSIRVQGRKVKAKSFFKLQ 127  
QY 110 -----LTLPELLADTRVTQSSIRTPWGISACLSFSGHAN--RFDGSNSTSHALLVI 160  
Db 128 SFDVSVKGISISVNLG--SESSOR-PTVTASSCS--SDIADVEVDSGGLGNLLNLF 181  
QY 151 ---VQHKIANVSNKCLISNLVQ--VNVHIGTIGLNPVGPESQIRYSMVSVPTVTS 216  
Db 182 HNQIESKFKVLESRICEMIKSVSSDLQYLPQLTPVTEIDSFADIDYSLVEAPRATAQ 241  
QY 217 YISLEVNALP-----LLGKEIILPTDATPFLPHVGTGEGMATVGLSQQLFDSA 267  
Db 242 MLEVNFKEIFHRNRSPTVLLAAVMSUPEE-----HNKMVYFAISDYVFNTA 289  
QY 268 LLLQKAGALNDIT--GQLRSDNL--LNTSALGRILPEVARQPPMPVVLKVRIGATPV 325  
Db 290 SLVTHEEGYLNFSITDDMPDPSNIRLT--KSPRPVPLRLALYPN-MNLELQ---GSVPS 345  
QY 326 A-MLHTNNATRLQPFVEV--LATNSAFQSLPSLDVVVNNRLQLSVKVQLQGTTSVL 382  
Db 346 APLNFSFNGLSVDPMEDAFVLLPSSSGKEPVRLSVATNVSATLTNTSKITGFLKP- 404  
QY 383 GDVOLTVAASNNGFIDTQVRLMGTVFEPKPLDHLNALLAMGIALPGVNNLHYVAPEIF 442  
Db 405 GKVKVELKESKVLGNFAELLEALLNYILNTPYKFNDKLAEGFPLPLKRVQLYDLGLQ 464  
QY 443 VYEGYVWISSGLFY 456  
Db 465 IHKDFLFLGANVQY 478

## RESULT 5

B35843  
lipopolysaccharide-binding protein - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 05-Oct-1990 #sequence\_revision 05-Oct-1990 #text\_change 20-Aug-1999  
C:Accession: B35843; A46553  
R:Schumann, R.R.; Leong, S.R.; Flaggs, G.W.; Gray, P.W.; Wright, S.D.; Mathison, J.C.; Science 249, 1429-1431, 1990  
A:Title: Structure and function of lipopolysaccharide binding protein.  
A:Reference number: A35843; MUID:90365281; PMID:2402637  
A:Accession: B35843  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-482 <SCH>  
A:Cross-references: GB:M35534; NID:G135467; PIDN:AAA99235.1; PID:G165468  
R:Tobias, P.S.; Soldau, K.; Ulevitch, R.J.  
J:Exp. Med. 164, 777-793, 1986  
A:Title: Isolation of a lipopolysaccharide-binding acute phase reactant from rabbit serum  
A:Reference number: A46553; MUID:8635528; PMID:2427635  
A:Accession: A46553  
A:Molecule type: protein  
A:Residues: 27-55, 'X3', 58-62, 'F', 64-65 <TOB>  
C:Superfamily: lipopolysaccharide-binding protein  
C:Keywords: acute phase

Query Match 11.1%; Score 251; DB 2; Length 482;  
Best Local Similarity 25.0%; Pred. No. 3.2e-11;  
Matches 125; Conservative 88; Mismatches 219; Indels 68; Gaps 22;  
QY 3 WASRL--GLLLALL--PVGASTPTGVRLNKAALSYVSEIGKAPLQ-RALQVTPF-- 54  
Db 4 WARALLGSTLLSLLLAAPGALG--ENFLITRTDKGLEVAAREGLLALQRLLEVLPDS 63  
QY 55 -----HFLDWSGEALQPTRIK--LNVHVPRLH-----LKFIAGFVRLAAANF-- 97  
Db 64 DGDGRIKHP--GRA---QVKYSLKIPRELLRGTLRPLPGQGLSLDISDAYIHVRG 115  
QY 98 TKVFPRAPEPLE-----LTPVELLADTRVTQSSIRTPWGISACLSFSGHAN-BF 147  
Db 116 SMKVRKAFRLKNSFDLYVKGLTISVHLVIG--SESSOR-PTVTSSCS--SDIQNVEL 169  
QY 148 DGSNSTSHALLVQHKIKA---VLSNKLCLISNLVQGVNVHIGTIGLNPVGPE--- 200  
Db 170 DIEGDLLE-LNLLQSQIDARLEVLKSKIQIE---EAVTALQPYQLTPVTQIDS 225  
QY 201 -SQIRYSMVSVPTVTSYISLEVNALVFLGKPIILPTDATPFLPHVGTGEGMATVGL 259  
Db 226 FAGIDYSLMEAPRATAGMLDMVKGEIIFPLDHRSPVDFLAPAMNLP--AHSRMVFSI 282  
QY 260 SQQLFDSALLLQKACALNDIT--GQLRSDNLNLTSAIGR-LIPEVARQPPMPVVLK 317  
Db 283 SDYVENTASLAVHKSGYWNFSITDAMVPADLNIRRTKSPRPVPLLANLYPN-MNLELQ 342  
QY 318 VRLGATPVAMLHTNNATRLQPFVEVLATNSAFQSLPSLDVVVNNRLQLSVKVKLQ 377  
Db 342 GTVNSEQLVNLSTENLEPEMCEALVVLPSAREPVFLGVATNVSATLTNTKTIKG 402  
QY 378 TTSVIGDVLQTVASNVGPIDTCQVRLMGTVFEPKPLDHLNALLAMGIALPGVNNLHYV 437  
Db 402 FLKP-GRQLVKEKSKVGQFNVELLEALLNYILNLYPKVNEKLAHREFPLPLRHILQY 460  
QY 438 APEIFVYEGYVWISSGLFYQ 457  
Db 461 DLLLQTHENFLLVGANIQIR 480

## RESULT 6

S10180  
bactericidal permeability-increasing protein precursor - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 20-Aug-1999  
C:Accession: S10180  
R:Leong, S.R.; Camerato, T.  
Nucleic Acids Res. 18, 3052, 1990  
A:Title: Nucleotide sequence of the bovine bactericidal permeability increasing protein  
A:Reference number: S10180; MUID:90277418; PMID:2349103  
A:Accession: S10180

A:Molecule type: mRNA  
A:Residues: 1-482 <LEO>  
A:Cross-references: EMBL:X52563; NID:g138; PID:CAA36797.1; PID:g139  
C:Superfamily: lipopolysaccharide-binding protein  
F:1-26/Domain: signal sequence #status predicted <SIG>  
F:27-482/Product: bactericidal permeability increasing protein #status predicted <MAT>  
Query Match 10.9%; Score 247.5; DB 2; Length 482;  
Best Local Similarity 22.6%; Pred. No. 5.9e-11;  
Matches 121; Conservative 98; Mismatches 224; Indels 61; Gaps 16;  
QY 3 WASRLGLLALLPVGASTPGTVRLNKAALSYVSEIGKAPLQALQ-VTVPHF-----56  
Db 11 WATL-VWLAAGTAVTTTPGIVARITQKGLDYACQGVLTQKLEKTIIPFSGNFK 68  
QY 57 LWSGEA-----LQPTRIRILNVHVRILHLKFIAGFGRV---LAAA 95  
Db 69 IKYLGKQYFFSMVIOGFNLNSQIRPLDKGLDSIRDASIKIRCKWKARKNFIXLGG 128  
QY 96 NETFKYFRAPELELTLPVELLADTRVTSQSIPTPVVSIACSLFSG-HANEFQGSNSTS 154  
Db 129 NFDLSV-----EGISILAGNLGYPASGHST-----VTCSSCS--SGIN-VRIHISGSL 177  
QY 155 HALLVLVQKHIAVL-----SNKCLSTSNLVQGV-VNVHLGTGLGLNPVGESQIRYSWVS 209  
Db 178 GMLIQLFKRIEISLQKSMTRKICEVTVSVSSKAPYFOTLPVTKLDKVGVDVSLVA 237  
QY 210 VETVTSQY:SLVNAVILFLG-----KPIILPTDTPFVLPRHVGTEGSMATVGLSQOLF 265  
Db 238 PPRATANLNDLWLLKGEFFSLAHSRSPPPFAPALAF-----SDHRRVYVLSISYFFN 290  
QY 266 SALLILQKAGALNDITGOL--RSDNLTNTSALGLIPEVARQPPPEPMPVVLKVLGAT 323  
Db 291 TAGFVYQKAGALNTRDDIMPKESFRITTKFFGLIPQVAKMFPD-MQMQLFIWASLP 349  
QY 324 PVAMLHTNNATLRQPFVEVLATASNAPQSLFSDVNVNLRQLSVSKVKGTTSVLG 383  
Db 350 PKLTWKPSLLDIFVLDTQAFALLPNSLDPLLEMLNLSVVGAKSDRLIGELR-LD 408  
QY 384 DVQLTVASNVGFIIDQVRLTGMVTFKELDLHALLAMGLALPGVNVLEVVAPEIFV 443  
Db 409 KLLLEKHSIDGFFSVESLQSVINYVMTIVLPVINKKQKGFPLPAYIELFNLTLP 468  
QY 444 YEGYVVISGLPY 456  
Db 469 YCDFLLFGADVQY 481  
RESULT 7  
I56246  
lipopolysaccharide binding protein - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 20-Aug-1999  
C:Accession: I56246  
J.Su, G.B.; Freeswick, P.D.; Geller, D.A.; Wang, Q.; Shapiro, R.A.; Wan, Y.H.; Billiar, J.; Immunol. 153, 743-752, 1994  
A:Title: Molecular cloning, characterization, and tissue distribution of rat lipopolysaccharide-binding protein  
A:Reference number: I56246; PMID:94292804; PMID:8021509  
A:Accession: I56246  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-481 <RES>  
A:Cross-references: GB:L32132; NID:g510714; PID:AAA21835.1; PID:g510715  
C:Superfamily: lipopolysaccharide-binding protein  
Query Match 10.9%; Score 246.5; DB 2; Length 481;  
Best Local Similarity 24.6%; Pred. No. 6.9e-11;  
Matches 121; Conservative 79; Mismatches 210; Indels 81; Gaps 21;  
QY 7 LGLLALLLPVVGASTPGTVRLNKAALSYVSEIGKAPLQALQ-VTVPHFLDWSGE---62  
Db 13 LGLLL-LSPRTQGVNPAWVRITDKGLEVAAGKGLLSQRELYKITLP---DFSGDPKI 68

QY 63 -----ALQPTRIRILNVHVRILHLKFIAGFGRV-----LAAAFTEKVFRAPEPL----108  
Db 69 KAVGGQYEHSLIQLSCQAGSSILKPLFGAGLSLSDSSISVGRKWKVRRSFVKLHGS 128  
QY 109 -----ELTLPVELLADTRVTSQSIPTPVVSIACSLFSGHAN-----EPDGSNSTSHAL 157  
Db 129 FDLVKSVTISVDLLGVDPSE-----RPTVTASCS-----NRIRDLELHVSNGVGMLL 178  
QY 158 LVL---VQKHIAVLSNKLCLSLSNLVQGV-----VNVHLGTGLGLNPVGESQIR 204  
Db 179 NLFINQIESLQKLVESKICEMIKSVTSILOPYLQTLPTVADIDTILGID-----229  
QY 205 YSMVSVPTVTSQYSLSEVNAVIFLLG--KPIILPTDTPFVLPRHVGTEGSMATVGLSQ 262  
Db 230 YSLVAAQPAQAQTLDVMEKEIFENENRSPTVTEPT--MSLPE---DSKQVTFALSDQ 284  
QY 263 LFSALLLQKAGALNDIT--COLRSDNL--LNTSALGLIPEVARQPPPEPMPVVLKVL 320  
Db 285 AFNATRVVHQAGYLNFTITDEVLPPDSNIRLNTKAPRPTPLITRKYPD-MNELLGTV 343  
QY 321 GATPVAMLHTNNATLRQPFVEVLATASNAPQSLFSDVNVNLRQLSVSKVKGTT 380  
Db 344 VSAPLNVSPGNLSLAPQMEIEGFVILPSSARESVPRLGVTVNVFSLTFDNSKVTGMH 403  
QY 381 VLGDVQLTVASSNVGFIIDQVRLTGMVTFKELDLHALLAMG--LALPGVNVLHVVA 438  
Db 404 P-EKAQVRLIESKVGMEVNVLFAPLNYLLNSLYPDVDELAKGFFPLPRRICKHDL 462  
QY 439 PEI---FVTEG 446  
Db 463 FOIKHNFYLG 473

## RESULT 8

A35843  
lipopolysaccharide-binding protein - human  
C:Species: Homo sapiens (man)  
C>Date: 05-Oct-1990 #sequence\_revision 05-Oct-1990 #text\_change 20-Aug-1999  
C:Accession: A35843  
R.Schumann, R.R.; Leong, S.R.; Flagg, G.W.; Gray, P.W.; Wright, S.D.; Mathison, J.C.; Science 249, 1429-1431, 1990  
A:Title: Structure and function of lipopolysaccharide binding protein.  
A:Reference number: A35843; PMID:90335281; PMID:2402637  
A:Accession: A35843  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-477 <SCH>  
A:Cross-references: GB:I35533; NID:g186965; PID:AAA59493.1; PID:g186966  
C:Genetics:  
A:Gene: GDB:ILBP  
A:Cross-references: GDB:131571; OMIM:151993  
A:Map position: 20q11.23-20q12  
C:Superfamily: lipopolysaccharide-binding protein  
Query Match 10.6%; Score 241; DB 2; Length 477;  
Best Local Similarity 23.7%; Pred. No. 1.8e-10;  
Matches 115; Conservative 93; Mismatches 219; Indels 59; Gaps 22;  
QY 9 LLLALLL---PVVGASTPGTVRLNKAALSYVSEIGKAPLQ-RALQVTVPHFLDWSGEAL 64  
Db 11 LLLALLLSTPEALGANFLVARITDKGLQYAAQEGLLALQSELLRITLP---DFTGDIR 67  
QY 65 QP-----TRIRILNVH-VPRJH--LKFIAGFGRVRLAA-----ANFTFKVFRAPEPLE- 109  
Db 68 IPHVGRGRYEHSLNIHSCELLHGAIRPVPQGLSLSDSSIRVQGRKWKVRSFKKQ 127  
QY 110 -----LTPVELLADTRVTSQSIPTPVVSIACSLFSGHAN--EPDGSNSTSHALLVL 160  
Db 128 SFDVSVKGISISVNLGL---SESSGR-PTCYCLSCS--SDIADVEVDMVSGDWGLNLF 181  
QY 161 ---VQKHIAVLSNKLCLSLSNLVQGV-VNVHLGTGLGLNPVGESQIRYSWVPTVTS 216  
Db 182 HNQIESKQVLESRICEMIQKVSVDLPYLTPTVTTEIDSPADIDYSLVAPRAQAQ 241



RESULT 11:  
 S43383  
 bactericidal/permeability-increasing protein - synthetic  
 C:Species: synthetic  
 A:Note: Homo sapiens (man) gene engineered and expressed in *Escherichia coli*  
 C:Date: 20-Oct-1994 #sequence\_revision 15-Feb-1996 #text\_change 15-Feb-1996  
 C:Accession: S43383  
 B:Qi, S.Y.; Li, Y.; O'Connor, C.D.  
 Biochem. J. 298, 711-718, 1994  
 A>Title: The region around residue 115 of human bactericidal/permeability-increasing protein of a gene coding for the active domain and characterization of recombinant proteins.  
 A:Reference number: S43383  
 A:Accession: S43383  
 A:Molecule type: DNA  
 A:Residues: 1-250 <QIS>

Query Match 5.8%; Score 132; DB 4; Length 250;  
 Best Local Similarity 21.7%; Pred. No. 0.013;  
 Matches 50; Conservative 54; Mismatches 98; Indels 28; Gaps 10;

QY 23 PGTVRLNKAALSYSEIGKAPLQAL-QVTPHFLD-----WSGEALQPTTR 70  
 DB 4 PGVVRISSQGLDYASQOQTAAQLKELRIKIPDYSDFKIKHLKGHSYFMDIREFQ 63  
 QY 71 ILNVH---VPRHLKLF-IAGFGVRLAAANFTKVFRAPEPLETLF-VELLADTRV-TQ 124  
 DB 64 LPSSQISVVPVNGLKFSISNANIKISGKWKAKRFLKMGNGFDJSTEGKWSISADLKGSN 123  
 QY 125 SSIRTPVVISACSLFSGHANFPGDSNSTSHA--LLVLVQKHKAVLSNKL-----CLIS 178  
 DB 124 PTSGKPTITCSC--SSHINSVHVHISKVGMILQLFHKIESALENKNSQVCEKVT 180  
 QY 179 NLVQG-VNVHLGTLGLNPGVPSQIRYSMVSVTPTSDYISLEVNALVF 227  
 DB 181 NSVSSKLQVPQTLEVMTKIDSVAGINVLVAPPATTAEITLDVQMKGEFY 230

RESULT 12  
 T22700  
 hypothetical protein F55B12.5 - *Caenorhabditis elegans*  
 C:Species: *Caenorhabditis elegans*  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 04-Mar-2000  
 C:Accession: T22700  
 R:Sim, M.  
 submitted to the EMBL Data Library, September 1996  
 A:Reference number: Z19602  
 A:Accession: T22700  
 A>Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-576 <WIL>  
 A:Cross-references: EMBL:Z75757; PIDN:CA802126.1; GSPDB:GN03023; CESP:F55B12.5  
 A:Experimental source: clone F55B12  
 C:Genetics:  
 A:Gene: CESP:F55B12.5  
 A:Map position: 5  
 A:Introns: 47/1; 147/3; 178/3; 290/3; 353/2; 384/2; 427/3  
 C:Superfamily: *Caenorhabditis elegans* hypothetical protein F55B12.5

Query Match 5.8%; Score 132; DB 2; Length 576;  
 Best Local Similarity 21.2%; Pred. No. 0.042;  
 Matches 106; Conservative 72; Mismatches 208; Indels 114; Gaps 20;

QY 24 GTVRLNKAALSYSEIGKAPLQALQVTPHFLDWSGEALQPTTRILNVHPRHLKLF 83  
 DB 32 GIYRLNKAALSYSEIGKAPLQALQVTPHFLDWSGEALQPTTRILNVHPRHLKLF 83  
 QY 84 IAGFGVRLAAANFTKVFRAPEPLETLFV-----ELLADTRVTSQIRTEV 131  
 DB 90 IDCKGV-----AYNISLAFRASAVAEISVFWMSVEGDTAELELSIESEHLFDYNGTTT 145  
 QY 132 YSISACSLFSGHANFPGDSNSTSHALLVIVQKHKAVLSNKLCLISNLVQGVNHLGTL 191  
 DB 146 VNASVCNVTHSELSLVFPFGSSLSALQSEIKQIVSALRDAVC---TTAVEA---LTFV 199

QY 192 IGLNVPVGPES-----QIRYSMVSVPTVT--SDYISLEVNALVFLLLGKP 232  
 DB 199 MAQKIPPEPPSPYKPEACDPKSGFSAELGASLCQVDVTWVGFEDESGEENGVETTVAPTP 258  
 QY 233 ----IILPTDAPFVLPVHVGTEGSM-----ATVGLSQQLFDSALLL--LQKAGA 276  
 DB 259 DDNSTLTATEEQ---KSYWGVLDLSVNHPPPTFDEDMITGL-----DGGILFNGWKADSA 310  
 QY 277 LNLDTTGLRSDNLLNTLSALGRLLPEVA-----ROPPEPMPVVLKVLGA 322  
 DB 311 QQLQILNKIRLDKKGVI-LSEYIPNTLFHHIYWDLGNFKHRTTPSPLPKILQ-KLSK 368  
 QY 323 TPVAMLHTN-NATLKLQPFVEV-----LATASNAFQSLFSLDVVNLRLQLSVSK 372  
 DB 369 AVCSKCYVEVSANLTEQILQIDAHLGARVOLSGNVSMFHGREGQLHDVHLHANTKLHVTL 428  
 QY 373 VKLQTTSVLGDVQLTVASSNVGFIDTQVRLMTGVTFEKLPLDLNAL-----LA 423  
 DB 429 KFTVHRSIFGDSVLTNVVNVFVDSCTQ-----EKLTKNFSCINLKVEQKFLQJG 479  
 QY 424 MG--IALPGVNVNLYVAPEI 441  
 DB 480 LGGPLAAPLEKLFSEFVPRV 499

RESULT 13  
 C86183  
 hypothetical protein [imported] - *Arabidopsis thaliana*  
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)  
 C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
 C:Accession: C86183  
 R:Theologis, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, N.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Huizar, L.  
 Nature 408, 816-820, 2000  
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A:Authors: Salzberg, S.L.; Schwartz, J.C.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A>Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.  
 A:Reference number: A86141; MUID:21016719; PMID:11130712  
 A:Accession: C86183  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-488 <STO>  
 A:Cross-references: GB:AB005172; NID:g7211993; PIDN:AAF40464.1; GSPDB:GN00141  
 C:Genetics:  
 A:Map position: 1

Query Match 5.3%; Score 120.5; DB 2; Length 488;  
 Best Local Similarity 18.2%; Pred. No. 0.24;  
 Matches 94; Conservative 105; Mismatches 205; Indels 113; Gaps 22;

QY 7 IGLILLA--LILPVVGASTPG-TVRLNKAALSYSE--IGKA-----PLQ-----RALQV 51  
 DB 8 LFLLLPSFFFLPSQTQSTDSFTSVLSQNGLDVFNLLVKNKAIASIIPLQIPRIEKSMKI 67  
 QY 52 TVPHFLDWSGEALQPTTRILNVHPRHLKLFAGFGVRLAA--NFTPAVF 102  
 DB 68 P---FL--GGIDVVNMLTYELDVASSYVK-IGETGVIVASGTTNLSNMWHYSYTW 121  
 QY 103 RAP-----EPLELTPEVLLADTRVTSQIRTPVVSISACS----- 138  
 DB 122 LPPIEISDQIASVQVQGEIGLSGLKSD-----EGSLK--LSLSFGCHVEDITIELE 174  
 QY 139 ----LFSGHANFPGDSNSTSHALLVIVQKHKAVLSNKLCLISNLVQGVNHLGTLIG 193  
 DB 175 GGASWFIYQGVNNAFKDQIGSS-----VESTIAKLTGEGVSDI---DSFLQSLPK 220  
 QY 194 LNPVGPESQIRYSMVSVPTVTSDYISLEVNALVFL-LGKP-----LILPTDA 239

Db 221 EIPVDNADLVNFTSDPILNRSSITFEIDG-LFTKGETNQVLKSPFKSVSLVIPCNGS 279  
 QY 240 TPFVLPVRHVGTEGSMATVGLSQOLFDSALLLQKAGALNDITGQLRSDNLLNTSALGR 299  
 Db 280 -----KMLGTSVDRAVFNAAALYNADFQGVV--DKIPQSLLNTARWRF 324  
 QY 300 LIPEVAROFFEPMFVVLKVRLGATPVAMLHTNATLRLQPFVEVLATASNAFQSLFSLD 359  
 Db 325 IIPQYKKYPN-QDMNLNISLSPPLVKISEQVGVANVADLVINVLDAQVI-PVACIS 382  
 QY 360 VVWNLRLQLSVKVQLQTTSLVGLQVLTAVSSNVGFIIDQVRLMGTVFEKPLDLHLN 419  
 Db 383 LMIKSGALRWGNLNGSVS-LEDFMSLKWNSIGNLHLHLQPIVMTVIQTVPVYAN 441  
 QY 420 ALLAMGIALPFGVNLHYVAPEIFVVEGVVVISGLFY 456  
 Db 442 DHLEKGFPEIMHGFTLQNAELICSESEITVCSDAY 478

RESULT 14  
 T29190  
 hypothetical protein C55C3.1 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C:Accession: T29190  
 R:Wessene, J.; Stellyes, I.  
 A:Submitted to the EMBL Data Library, April 1996  
 A:Description: The sequence of C. elegans cosmid C55C3.  
 A:Reference number: Z20585  
 A:Accession: T29190  
 A:Status: Preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-606 <WQE>  
 A:Cross-references: EMBL:U53335; PIDN:AAA96173.1; GSPDB:GN00022; CESP:C55C3.1  
 A:Experimental source: strain Bristol N2; clone C55C3  
 C:Genetics:  
 A:Gene: CESP:C55C3.1  
 A:Map position: 4  
 A:Introns: 61/3; 99/2; 126/2; 161/3; 283/2; 359/2; 424/1; 463/3; 522/1; 570/1

Query Match 5.1%; Score 116; DB 2; Length 606;  
 Best Local Similarity 21.2%; Pred. No. 0.73;  
 Matches 105; Conservative 76; Mismatches 186; Indels 128; Gaps 25;

QY 13 LLLPVGASTPGTVRLNKAALSVEIGKAPLQRA-----LQVTPHFLDMSGEALQPTR 68  
 Db 74 LLLPDVEHILP-----SNQGIIVISKVLSRFAEHQNLSTAPNKSIT--MQNMD 124  
 QY 69 IRLNVHVRHLKFIAGFGVRLAANFTKVPRAPELTLPLVELLAD--TRVTQSS 126  
 Db 125 IGLLG-----DLSSGVNVV-----PLNLTGQVELLAQGLTFHLESS 161  
 QY 127 IR-----TPVVISISACSLF-----SGHANEFDG-----SNSTSHALLVL--V 161  
 Db 162 IEKNGSAKVTSLSCATRDVTWTHNGGLFGLAVSFQGVSDNVRHMLQTIICKV 221  
 QY 162 QKHKAVLSNKL--CLSSINLVQGVNHLGTLGLNVPGPSQIRYSNVSV-----210  
 Db 222 RKYIDEDANEKLAESAQTSSKLADALETNALQWIS--VGGDEKSRIDISSIFDSSLASKF 278  
 QY 211 -----TPTVSDYISLEVNALVELLQK--PIILPTDA-----TPPV--LPRHVGTEG 252  
 Db 279 FIDFRLKEHPICOENTVELASWGISFMGQGDTPFGVDASWPGRSPPKTNVVDVSTNKC 338  
 QY 253 SMATVGLSQOLFDSALLLQKAGALNDITGQLRSDNLLNTSALGR-----LIPVYARQ 307  
 Db 339 SMIELVSDLPNLSLLHYAVQRIKVLPRTKGVSSFLATTCGSEFCISDLAPLAEQ 398  
 QY 308 FPEPMFVVLKVRGAT--PVAMLHTNNA-----TLRLQPFVEVLATASNAFQSL--FSLDVV 361  
 Db 399 YPNS---TVELAMSATRAPVLPEKNGGTISVSLGLVGVVFAVNGNQRRQVIVVDLDVV 455  
 QY 362 VNLRLQLSVKVQLQTTSLVGLQVLTAVSSNVGFIIDQVRLMGTVFEKPLDLHLN 414

Db 456 ADARL-----SIQG-HNVSSGVELRKFDLKRKTGTVDISDAEIDDIALLVSQLSE--- 504  
 QY 415 LOHLNALLAMGIALP 429  
 Db 505 -KLLNGLLVNGMPEIP 518

RESULT 15  
 A90140  
 conserved hypothetical protein [imported] - Sulfolobus solfataricus  
 C:Species: Sulfolobus solfataricus  
 C>Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 24-May-2001  
 C:Accession: A90140  
 R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-  
 Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.  
 arrett, R.A.; Ragan, M.A.; Sersen, C.W.; Van der Oost, J.  
 A:Submitted to GenBank, April 2001  
 A:Description: Sulfolobus solfataricus complete genome.  
 A:Reference number: A99139  
 A:Accession: A90140  
 A:Status: Preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-974 <KUR>  
 A:Cross-references: GB:AE006641; NID:gl13813136; PIDN:AAK40376.1; GSPDB:GN00155  
 C:Genetics:  
 A:Gene: SSO0011

Query Match 5.0%; Score 113; DB 2; Length 974;  
 Best Local Similarity 20.0%; Pred. No. 2.4;  
 Matches 99; Conservative 78; Mismatches 217; Indels 100; Gaps 21;

QY 13 LLLPV-VGASTPGTVRLNKAALSVEIGKAPLQRAQVTPHFLDMSGEALQPTRIRI 71  
 Db 250 VLVPIDIGSSNQ---VSLEDAGWTPSDDEWAPGETLFLTI--YVKNLGENLLSNVMLI 304  
 QY 72 LNVHVRHLKFIAGFG-VRLAANFTF-----KVFRAPELELTLPVELLADTRVTS 125  
 Db 305 LQSHVP---IQFLQNYTMIGFVAGGYNVTVVANYKNVTPGVYVYVITLVAYDGGFMQ 361  
 QY 126 SIRTPV-----VSISACSLFSGHAN-----BPDGNSNSTSHALLVQK 163  
 Db 362 TFEPMFVVLGVNFSASSVMGTTSNPMVWGPGENNIPILTIILQNGSIVTVTNATLFLQSQ 421  
 QY 164 HIKAVLSNKLCLSLNVLQGVNHLGTLGLNVPGPSQIRY-----SNVSV 211  
 Db 422 YPVQFLQNN--VTLGNVPAGYPIPVTVLANVPNTNVTGVIYITAKWYVDGVIQVVKVS 479  
 QY 212 TPTSDYISLEVNALVELLQKPIILPTDATPFVLPVRHVGTEGSMATVGLSQOLFDSALLIL 271  
 Db 480 IYIESLNQSVSEGIWGLSNFIL-----VAPGENNVPLTLVKNLGENLSNVSLIL 531  
 QY 272 QKAGALNDITGQLRSDNLLNTSALG-----RLIPEVAROPPEPMFVLKVRGATP 324  
 Db 532 QSHYPIQF-----LQNASVGVPAGSYNYVTVTANVPNATPGVYI-----P 575  
 QY 325 VAMLHTNATLRLQPFVEVLATASNAFQSLFSDVNVNLRQLSVSKVLQGTTSVLGD 384  
 Db 576 ATLVAVGKPKENIMTVDILGYVTIQ--QSLWG-----EVTSPITVS-----SGET---D 621  
 QY 385 VQLTVASSNVGFIIDQVRLMGTVFEKPLDLHLNALLAMGIALPGVNVNHYVAPEIF-- 442  
 Db 622 VPLTVLLKNTGDVNLINA-TLVFQNVVEPLIFH-QATAQIGIVPAGQENYATVTVSFPN 679  
 QY 443 VYEGVYVVISGLFY 456  
 Db 680 ATPGVYVYIPATLYY 693

Search completed: June 29, 2004, 11:00:55  
 Job time : 23 secs





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Db      6 LLALLAVISLTAASPGVKVLTDKGIEYKGQIGMASLQOKLTKMKVP---DLSGTEKVP 62
Qy      56 P-----TRIRLVHVRHLKFIAGFGVRLAA-----ANFTFKVFR----- 103
Db      63 PIKVKYSLTGMIVNLGLPKSALVLMFGTGVRLAINTAFINLHGNWRVRFRIQDRGS 122
Qy      104 ---APELELTLPVELLADTRVTOSSIRTPVVISASCSLFSGHAN-BFDGNSNSTHALL- 158
Db      123 FDLAVNGLTIT-----ADIAIKSDETGRPTVSTVNCVANVGSASIKFHGGASWLYNLF 176
Qy      159 VLQKHKHKAIVLSNKLCLISNLVGVNVHGLTGLINPVGPEPESQIRYSMVSVPTVT 218
Db      177 SYDKALRSALQKQICPLVADITDMPHLKTNLVLAQVDAIEYSMTVSTPISKSI 236
Qy      219 SLENAVLFLLGKPIILPTDATPVLPRHVGTGSMATVGLSQQLFDSALLLQKAGAIN 278
Db      237 EFSLKGEFFYNIKGHQEPFPTPSLPQ---DNMLYIGVSSFTPSAGFVYNAGALS 293
Qy      279 LDTIGQL--RSDNMLNTSALGRLIPEVARQFPPEPMPVVLKVLGATPVAMLHTNNATLR 336
Db      294 LYVTDDMIPPSSPIRLNTGTGFGVPEIAKRFPG-MMMKLLVKTVEKPTISLEPNVTWQ 352
Qy      337 LQPEVEVLATASAFQSLFSLDVVNLRLQLSYKVKLQCTTSVLGDVQLTVASSNVGP 396
Db      353 ASGTVTAYAIQPNNTLSPLFVLNMEGVSQMNVTGKLAGAIT-LNKIENTLTGTSYVQ 411
Qy      397 IDTDQVATLMTGTVPEKELDLHLNALLAMGIALPGVNLHLYVAPEIFVYEGVWISS 452
Db      412 FVQGSLDNIFLVLKVVIPKVNARLEKGPFP-PTIGKMNLLNTQLVLKQVLMIGT 467

RESULT 2
Q80FX4
ID      Q80FX4      PRELIMINARY;      PRT;      473 AA.
AC      Q8JFX4
DT      01-JUN-2003 (TrEMBLrel. 22, Created)
DT      01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT      01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE      LBP (LPS binding protein)/BPI (Bactericidal/permeability-increasing protein)-1.
DE      LBP/BPI-1.
GN      Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC      Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX      NCBI_TaxID=8022;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      MEDLINE=2203144; PubMed=12033361;
RA      Inagawa H., Honda T., Kohchi C., Nishizawa T., Yoshiura Y.,
RA      Nakanishi T., Yokomizo Y., Soma G.;
RT      "Cloning and characterization of the homolog of mammalian
RT      lipopolysaccharide-binding protein and bactericidal permeability-
RT      increasing protein in rainbow trout Oncorhynchus mykiss.";
RI      J. Immunol. 168:5638-5644(2002).
DR      ENBL; AB042025; BAB91243.1; -.
DR      GO; GO:0008289; F:lipid binding; IEA.
DR      InterPro; IPR001124; LBP_BPI_CETP.
DR      Pfam; PF01273; LBP_BPI_CETP; 1.
DR      SMART; SM00328; BPI1; 1.
DR      SMART; SM00329; BPI2; 1.
SQ      SEQUENCE      473 AA; 51431 MW; 3F9DF180695CA3D7 CRC64;

Query Match      17.3%; Score 392.5; DB 13; Length 473;
Best Local Similarity      26.9%; Pred. No. 4.2e-21;
Matches 129; Conservative      94; Mismatches 232; Indels      55; Gaps      14;

Qy      9 LLALLPVGASTPGTVRLINKAALSYVSEIGKAPLQALQ-VTVPHFLDWSG-EALQP 66
Db      7 LALLALVFALATNPVGKVKLTKEGIEYKGQIGMASLQOKLTKMKVP---DLSGTERVAP 63
Qy      67 -----TRIRLVHVRHLKFIAGFGVRLAA-----ANFTFKVFR----- 103

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Db      64 IGKVKYSLTGTITVNLGLPYSAALVPTDGTISLITNAFISLHGNWKIRYLSFIKDSGSF 123
Qy      98 TFKVRAPELELTLPVELLADT--RVTOSSIRTPVVISASCSLFSGHANFDGNSNSTH 155
Db      124 DLEV-----DGLTVDSTITIKSDETGRPTVSSWNC-VANVGSASI-----KPHGGASWLY 172
Qy      156 ALL-VLQKHKHKAIVLSNKLCLISNLVGVNVHGLTGLINPVGPEPESQIRYSMVSVPTVT 214
Db      173 NLSAYIDKALRSALQKQICPLVADITDMPHLKTNLVLAQVDAIEYSMTVSTPIS 232
Qy      215 SDYISLVNAVLFLLGKPIILPTDATPVLPRHVGTGSMATVGLSQQLFDSALLLQK 274
Db      233 NASIDFSLKGEFFYNIKGHQEPFPTPSLPQV---NNMLYIGMSAFTTNSAGFVYNA 289
Qy      275 GAINLDTIGQL--RSDNMLNTSALGRLIPEVARQFPPEPMPVVLKVLGATPVAMLHTNN 332
Db      290 GALSXYITDDMIPPSSPIRLNTRTGFAPETIAKRFPS-MMMKLLVKTVEKPTIFFEPNN 348
Qy      333 ATLRQPFVEVLATASAFQSLFSLDVVNLRLQLSYKVKLQCTTSVLGDVQLTVASS 392
Db      349 VTQASGVTAYAIQPNNTLSPLFVLNMEGVSARLYVTGVLGAVT-LNKIENTLT 407
Qy      393 NVGEIDTDQVATLMTGTVPEKELDLHLNALLAMGIALPGVNLHLYVAPEIFVYEGVWISS 452
Db      408 YVGFQVRSLDNIFLVLKVVIPKVNARLEKGFELPSIGKGNLNTQLVLKQVLMIGT 467

RESULT 3
Q804Q9
ID      Q804Q9      PRELIMINARY;      PRT;      473 AA.
AC      Q804Q9;
DT      01-JUN-2003 (TrEMBLrel. 24, Created)
DT      01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Bactericidal permeability-increasing
DE      protein/lipopolysaccharide-binding protein precursor.
GN      BPI/LBP.
OS      Cyprinus carpio (Common carp).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Osteiophysi; Cypriniformes;
OC      Cyprinidae; Cyprinus.
OX      NCBI_TaxID=7962;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Sakai M., Kono T.;
RA      TISSUP-Head kidney;
RT      "Molecular cloning of a novel bactericidal permeability-increasing
RT      protein/lipopolysaccharide-binding protein (BPI / LBP) from common
RT      carp Cyprinus carpio L. and its expression.";
RL      Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR      ENBL; AU279378; BAG56095.1; -.
DR      GO; GO:0008289; F:lipid binding; IEA.
DR      InterPro; IPR001124; LBP_BPI_CETP.
DR      Pfam; PF01273; LBP_BPI_CETP; 1.
DR      Pfam; PF02886; LBP_BPI_CETP_C; 1.
DR      SMART; SM00328; BPI1; 1.
DR      SMART; SM00329; BPI2; 1.
DR      Signal.
FT      SIGNAL.
SQ      SEQUENCE      1      18      POTENTIAL.
Qy      9 LLALLPVGASTPGTVRLINKAALSYVSEIGKAPLQALQ-VTVPHFLDWSG-EALQP 66
Db      7 LVILNLVSATGTNAGYKVELTQKGEYKGQIGIASIQQLRTIKVP---DISGTEKVP 63
Qy      67 -----TRIRLVHVRHLKFIAGFGVRLAA-----ANFTFKVFR----- 103
Db      64 IGKVKYSLTGTITVNLGLPKSALVLPDGTGMLSIGNAYINLHGNWRVRLIKDSGSF 123

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QY 104 --APEPELETLFVVELLADTRVQSGIRTPVWSISACSLFSGHAN-EFDGNSSTSHALL-V 159
DB 124 DLAVSELTISTTAVMSD-----DTGHTVSMNCAATVGSVNVKFGGASWLYNLFSS 177
QY 160 LVQKHIAVSNKLCISLNSVQGVNHLGFLGLNPNVGPESQIRYSMVSVPTVTSYIS 219
DB 178 FINKALRNALQKQICPLVADSADINPHLKTNLVLAKVDQVAIEYSVMGSEVLSNTSID 237
QY 220 LEKNAVLFLLGKPIILPTDAPFVLPVHVGEGSMATVGLSQQLFDSALLLQKAGALNL 279
DB 238 LGUKGERYN-GQHKPEPSPFPFSLP---SODTMLYIGVSAFTINAGFVYNRAGALSL 294
QY 280 DITQQLSDDMI-----LNTSALGRILPVARQFPPEPMPVVLKVLGATPVAHLTNN 332
DB 295 YIT-----DEMIPSGSPRLNKTGFAFIPQIERKMPGLM-MKLLVETVKEPIVTFEPNN 348
QY 333 ATLRLQFVEVLATASNAFOSLSLSDVVNRLQLSVSKVLOGTTSVLGCVLTWASS 392
DB 349 MTVQASSTV-AYAIQPNSTLSPLFVLMLEVSSTHYYTELKLAGNVT-LNKINMSLAKS 407
QY 393 NVGFIDTQVRLTGMVTFEPELDDHALLAMGIALPGVNNLHVVAPEIFVYEGVWISS 452
DB 408 YVGFQVTSLDNIFTIVLKFAVPEKVNARLOEGYPLPAIGMMQVLNSQLKVLKYLIGT 467

RESULT 4
Q42273 O42273 PRELIMINARY; PRT; 440 AA.
AC O42273 1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DE Bactericidal permeability increasing protein/lipopolysaccharide
binding protein.
DE Temp.
GN TENP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=White leghorn; TISSUE=Brain;
RX MEDLINE=98173457; PubMed=9514522;
RA Yan R.T., Wang S.Z.;
RT "Identification and characterization of temp, a gene transiently
expressed before overt cell differentiation during neurogenesis.";
RL J. Neurobiol. 34:329-328(1998).
DR EMBL; AF029841; AAC14583.1; -
DR GO; GO:0008289; F:lipid binding; IEA.
DR InterPro; IPR001124; LBP_BPI_CETP.
DR SMART; SMC0329; BP12; 1.
SQ SEQUENCE 440 AA; 47435 MW; A46C2D7FP34F2686 CRC64;

Query Match 16.7%; Score 377.5; DB 13; Length 440;
Best Local Similarity 27.1%; Pred. No. 5.1e-20;
Matches 126; Conservative 82; Mismatches 216; Indels 41; Gaps 11;

QY 7 LGILLALLPVVGASTPCTVTVRLNKALSVYSBTKG---APLQALQVTVPH---FLDW 59
DB 1 MGALLALLDPVQTPADPCGGIILTPGLSUYAEVSKPHEAVLRLQDLMKPEPQTCSLAPW 60
QY 60 SGEALQPTRILNVHVRHLKFIAGFGVRLAAANFTFKVFRAP-EPELETLFVELLA 118
DB 61 S-----PAGTELPAKVADLMSVPEAGRL---GVEELRIAPLHTVMPVIRISIRA 111
QY 119 DTRVTSQIRTPVWSISACSLFSGHANFEDGNSSTSHALLMLVQKHIAVSNKLCISIS 178
DB 112 DLHYDMGPDGNLQLTLSACRTVQAQSTREAESKSRIL-----DKVVDVDMKLCIFYS 165
QY 179 KLVQGVNVHGLTGLGNPVGPESQIRYSMVSVPTVTSYISLEVNALFLGKPIILPTD 238
DB 166 KLLIFPNEQLMSLTALFPVTPNCLQYLALAAPVFSKQGIALLSLQTTTFQVAGAVVPVPS 225
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QY 239 ATPFVLPFHVGTEGSMATVGLSQQLFDSALLLQKAGALNLDTQQLRSDNLTNTSALG 298
DB 226 PVFSPMPELASTSTSHLILALSEHYFTSLYTLERAGAFNMTI-----PSMLATTALH 278
QY 299 RLIEVARQFPPEPMPVVLKVLGATPVAHLTNNATLRLQFVEVLATASNAFOSLSL 358
DB 279 QKITQVGSYLHEDLPIITLSAALRSSPVVLREGRALKL--FLTVHIGAGSPDFOSFLSV 336
QY 359 DV-VVNLRLQLSVSKVLOGTTSVLGVDQLTVASSNVGFIDTQVRLTGMVTFEPELIDH 417
DB 337 SADVTRAGLQSVSDTRMTAVIEDAELSAASNVGLVRA----ALLEELFLAPVCOQ 392
QY 418 LNA-----LLAMGIALPGVNNLHVVAPEIFVYEGVWISSGLFYQS 458
DB 393 VPANMODVLRGSHLPHMSHFTYTDVNVVVKDVVLPCKLKLR 437

RESULT 5
Q7T3Q8 Q7T3Q8 PRELIMINARY; PRT; 473 AA.
AC Q7T3Q8 2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Bactericidal permeability increasing protein/lipopolysaccharide
binding protein.
DE BPI/LBP.
OS Gadus morhua (Atlantic cod).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
OX NCBI_TaxID=8049;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Head kidney;
RA Stenvik J., Solstad T., Leiros I., Jorgensen T.O.;
RT "Cloning and analyses of the BPI/LBP gene of the Atlantic cod (Gadus
morhua L.) - Implications for the evolution of the immune system.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY102629; AAM52336.1; -
SQ SEQUENCE 473 AA; 51513 MW; 9471E26BC1016E8D CRC64;

Query Match 16.7%; Score 377.5; DB 13; Length 473;
Best Local Similarity 25.8%; Pred. No. 5.6e-20;
Matches 123; Conservative 100; Mismatches 209; Indels 45; Gaps 13;

QY 9 LLLALLLPVVGASTPCTVTVRLNKALSVYSIGKAPLQALQ-VTVPHFLDMSG-EALQP 66
DB 7 LALLALLPLALSANAGVKVLTQKGLDPGRELAVASLQKLMTHIKVP---DLGKERVKP 63
QY 67 -----TRIRLNHVRHLKFIAGFGVRLAAANF-----TFKVER----- 103
DB 64 IGKRVSVTEKRVVVKGLGPSAIGLVPTGFSLTITNAFLSHGVRVKYLRFKDRGSP 123
QY 104 --APEPELETLFVVELLADTRVTSQIRTPVWSISAC-SLFGHANFEDGNSSTSHALL-V 159
DB 124 DLAKSLSIITTSISLSD-----NMGLPAMVAMASCITTLGGVSVKLGHGASWLYNLFRR 177
QY 160 LVQKHIAVSNKLCISLNSVQGVNHLGFLGLNPNVGPESQIRYSMVSVPTVTSYIS 219
DB 178 FIEKGLSQKLCPLVAESVSSNMFKTKVMAVDRYAEIAPMVSSPDISSSIG 237
QY 220 LEVNALFLGKPIILPTDAPFVLPVHVGEGSMATVGLSQQLFDSALLLQKAGALNL 279
DB 238 LNLKGEFVNIGNHMEPPSPAPFLPNQ---EQSMYIIGLSAFTANSASFVYNKAGTSL 294
QY 280 DITQQL--RSDNLTNTSALGRILPEVARQFPPEPMPVVLKVLGATPVAHLTNNATLRL 337
DB 295 KITDMVPRSPIRLTNTTFCGL-PQIAKLPPGLM-MVLQLKMTKDPILSSIEANKVTYDA 353
QY 338 QPFVEVLATASNAFOSLSLSDVVNRLQLSVSKVLOGTTSVLGVDQLTVASSNVGFI 397
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Db 354 KSSLTAYAILANTKLAPFLVNLDFSVSARVNVGNKLAGAVT-LNRIDMSLGKSYVGDF 412  
 QY 398 DTCQVRLTMCVTEKPKLLDHLNALLAMGIALPGVNLHYVAPLFFVVEGYVTVSSGL 454  
 Db 413 KVSLSNIFQIVLKVWVLPVTVNVLKEGFFPLSLGKLNKNTQILKGYIMIGTDL 469

RESULT 6  
 Q7T3Q9 PRELIMINARY; PRT; 473 AA.  
 AC Q7T3Q9;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Bactericidal permeability increasing protein/lipopolysaccharide  
 DE binding protein.  
 GN BPI/LBP.  
 OS Gadus morhua (Atlantic cod).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.  
 OX NCBI\_TaxID=8049;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=Head kidney;  
 RA Stenwik J., Solstad T., Leiros I., Jorgensen T.O.;  
 RT "Cloning and analyses of the BPI/LBP gene of the Atlantic cod (Gadus  
 morhua L.) - Implications for the evolution of the immune system.";  
 RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY102628; AA052335; -;  
 DR EMBL; AY102628; AA052335; -;  
 SQ SEQUENCE 473 AA; 51485 MW; 1290836926853F8P CRC64;

Query Match 16.6%; Score 376.5; DB 13; Length 473;  
 Best Local Similarity 25.8%; Pred. No. 6.7e-20;  
 Matches 123; Conservative 100; Mismatches 203; Indels 45; Gaps 13;

QY 9 LLLALLLVVGASTPGTVVRLNKAALSYVSEIGKAPLQALQ-VTVPHFLDWSG-ELQP 66  
 Db 7 LALLAL-PLALSANAGVKVLTQGLDFGRELAVASLQKLMITKVP---DISGKRVKP 63  
 QY 67 -----TRILNVHVRLEHLKFIAGVGVLLAANF-----IFKVER----- 103  
 Db 64 IGKRVSVTEMNRVVKGLGPSAIGLVFGTGSILITNATLHGRWRVKYURFVKDGRSP 123  
 QY 104 --APELELTLPVELLADTRVTQSSIRTPVVSISAC-SLFSGHANEFDGNSNSTSHALL-V 159  
 Db 124 DLAIKLSITTSISLSD-----NMGLPAVAMASCTITLGGVSVKLGASMLYNLFRR 177  
 QY 160 LVQKHIAVLSNKLCLISNLVQGVNHLGLTGLNVPVGPESQIRYSMVSVPTVTSYIS 219  
 Db 178 FIEKGLSQLOKLCPLVAESVSMNQFLKTVNVMAPVDYAEIAYPMVSSFDISSSIG 237  
 QY 220 LEVNAVFLFLGKPIILPTDAPFFVLPRHVGEGSMATVGLSQQLFDGALLLLQKAGALNL 279  
 Db 238 LNIKGEFYNIGNHEPESPAPFELPQ---EQSMVLYIGLSAFTANASAFVYNAGTSL 294  
 QY 280 DITSQQL--RSDNLLNTSALGRILPEVARQPEPMPVVLKVLGATPVMALHTNNA 337  
 Db 295 KITDDMPRSSPIRLT--NTFGVLIPQIAKLPPGLM--XVLQKMTNDPLSSIEANKVTDA 353  
 QY 338 QPFEVLATASAFQSLFDVVNVLQQLSVSKVKLQGTTSVLGDVQLTVASNVGFI 397  
 Db 354 KSSLTAYAILANTKLAPFLVNLDFSVSARVNVGNKLAGAVT-LNRIDMSLGKSYVGDF 412  
 QY 398 DTCQVRLTMCVTEKPKLLDHLNALLAMGIALPGVNLHYVAPLFFVVEGYVTVSSGL 454  
 Db 413 KVSLSNIFQIVLKVWVLPVTVNVLKEGFFPLSLGKLNKNTQILKGYIMIGTDL 469

RESULT 7  
 Q8IW58 PRELIMINARY; PRT; 487 AA.  
 ID Q8IW58;  
 AC Q8IW58;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Similar to bactericidal/permeability-increasing protein.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RA Strausberg R.;  
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC040955; AAH40955.1; -;  
 DR GO; GO:0008289; F:lipid binding; IEA.  
 DR InterPro; IPR001124; LBP\_BPI\_CETP.  
 DR Pfam; PF01273; LBP\_BPI\_CETP; 1.  
 DR Pfam; PF02886; LBP\_BPI\_CETP; 1.  
 DR SMART; SM00328; BPI1; 1.  
 DR SMART; SM00329; BPI2; 1.  
 DR PROSITE; PS00400; LBP\_BPI\_CETP; 1.  
 SQ SEQUENCE 487 AA; 53880 MW; FE709D9317E5206D CRC64;

Query Match 12.7%; Score 287; DB 4; Length 487;  
 Best Local Similarity 22.6%; Pred. No. 3.6e-13;  
 Matches 110; Conservative 104; Mismatches 228; Indels 44; Gaps 17;

QY 3 WASRLGLLLALLLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQALQ-QVTVPHFLD--- 58  
 Db 15 WAS-LNVLVALGTAVTAANVPGVVVRSQKGLDVASQQTALQKELKRIKIPYSDSEK 73  
 QY 59 -----WSGEALQPTRIRILNVH---VPRHLKP-IGAGVGVLLAANFTKVFRAPE 106  
 Db 74 IKHLGKHYSFYSDMDIREFQLPSSQISWVPVVGKFSISNANIKISGKWKAKRFLKWSG 133  
 QY 107 PLELTLP-VELLADTRV-TQSSIRTPVVSISACSLFSGHANEFDGNSNSTSHA--LLVLVQ 162  
 Db 134 NFDLSIEGMSISADLKLGSNPTSGKPTITCSSC---SSHINSVHVHISKSKVGMILQLFH 190  
 QY 163 KHIAVLSNKL-----CLISNLVQGVNHLGLTGLNVPVGPESQIRYSMVSVPTVTSY 217  
 Db 191 KTIESALNKNQNSQVCEKTVNSVSKLQPYQTLPVMTKIDSVAGINYLGLVAPPATTAET 250  
 QY 218 ISLEVNVLFLGKPIILPTDAPFFVLPR--RHVTEGSMATVGLSQQLFDSALLLLQKAG 275  
 Db 251 LDVQMKGEFYSENH-----HNPPFPAPVMEFFPAHDMVMVYGLSDYFNTAGLVYQEAG 305  
 QY 276 ALNLDITQQL--RSDNLLNTSALGRILPEVARQPEPMPVVLKVLGATPVMALHTNNA 333  
 Db 306 VLKMTLRDDMIPKESKPRLLTKFTGLPEVAKFPN---MKIQHVSASTPPLHSVQPT 362  
 QY 334 TLRLQPFVEVLATA--SNSAFQSLFDVVNVLQQLSVSKVKLQGTTSVLGDVQLTVAS 391  
 Db 363 GLTYPADVQCAFVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGELK-LORLLLEKH 421  
 QY 392 SNVGIFDITDQVRLTMCVTEKPKLLDHLNALLAMGIALPGVNLHYVAPLFFVVEGYVTV 451  
 Db 422 SNIGFFPVELLQDLMNVIVPILVLPVNEKLGKGFPLTPARVOLYNNVLQPHQNLFLFG 481  
 QY 452 SGLFYQ 457  
 Db 482 ADVVYK 487

RESULT 8  
 Q8BSF3 PRELIMINARY; PRT; 486 AA.  
 ID Q8BSF3;  
 AC Q8BSF3;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE weakly similar to bactericidal/permeability-increasing protein precursor.

OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Epithelium;  
 RL MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium,  
 RA "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs";  
 RX Nature 420:563-573(2002).  
 DR EMBL; AK033770; BAC28468.1; -  
 DR GO; GO:0008289; P:lipid binding; IEA.  
 DR InterPro; IPR001124; LBP BPI CETP.  
 DR Pfam; PF01273; LBP BPI CETP\_1.  
 DR Pfam; PF02886; LBP BPI CETP\_C; 1.  
 DR SMART; SM00328; BPI1; 1.  
 DR SMART; SM00329; BPI2; 1.  
 DR PROSITE; PS00400; LBP BPI CETP; 1.  
 SQ SEQUENCE 486 AA; 54351 MW; 9D8F627EA5496D62 CRC64;

Query Match 11.2%; Score 253.5; DB 11; Length 486;  
 Best Local Similarity 22.4%; Pred. No. 1.2e-10;  
 Matches 113; Conservative 97; Mismatches 222; Indels 73; Gaps 18;

QY 1 MAWA-----SRGLLLALLPVVGASTPGTGVRLNKAALSYVSEIGKAPLQ-RALQVTVPHFELDSGEAL 64  
 DB 1 MTWAPDNVKNVKSALLLAIIGTALTAATDPGVAMISQKGLDFACQGVVLEKELQALS 60  
 QY 53 VPHELDWSG-----EALQPTRIRILNVHVRHLKFIAGPGVRL----- 91  
 DB 61 VP---DFSGVFKEIKHLGKGVSEFYEMAVDGFHPNPKIEMLPDGLRVEIKDASIKINGK 117  
 QY 92 -LAAANFTKVPRAPELELTIPVELLADTRVQSSIRTPVVISACSLFSGHAN--EFD 148  
 DB 118 WMSRKNP-----LKAGNFELSGQVSISTDLLIGSDSGHITTI--CSNCDSHIDSVHIK 171  
 QY 149 GSNSTSHALLVQKHKAVLSN----KLCLISNLVQGVNVHLGTGLGNFVGPESQI 203  
 DB 172 IGSXVLGLRLFRHKIKTSLSKNIYKICKIVRDSVSKLQPYLKLTSVITRVDVTSV 231  
 QY 204 RYMSVPTVSDYISLVNAVFLGLKPIILPTDTPFVLRHVGTEGSMATVGLSQOL 263  
 DB 232 DYS-LAPLTTMQFLEGQLKGEFFWRGHRDPLFIH--PPVM-RFVPNGAYMVCMGISDYF 288  
 QY 264 FDEA-LILQKAGNLDTGOLRSDN--LNTSALGRLIPEVARQPE-----PM 312  
 DB 289 FNTVLAQQSGTLLKWTGGQLSNRGRFQLNDFLRTPLPKVAKMFPBMGVQLLISAPV 348  
 QY 313 PVV-KVRLGATFVAMLHTNNATRLQPFVFLATASNSAFQSLFSDVV---VNLQLQS 369  
 DB 349 PVHLSIQ----PSGL--SFNPKLEQAFAV---VLPNASLVFLVLMVRRKTNASLEVD 398  
 QY 370 VSKVKLQGTTSVLGVQVLTASSNVGFDITDQVRLMGTVFEKPLLDHLLNALLANGIALP 429  
 DB 399 AENRVLGEMKLGSRWLELKEKSPFKEYLEDVINYLVSTLVLPKINERLRGFFLP 458  
 QY 430 GVNHLHYVAPEIFVYGVYVWISSGL 454  
 DB 459 LPAGIRSFHTFPYQNFLLLEADL 483

RESULT 9

Q8TCF0 PRELIMINARY; PRT; 477 AA.  
 AC Q8TCF0;  
 DT 01-JUN-2002 (Tremblrel. 21, Created)  
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
 DE Lipopolysaccharide binding protein.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 CX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RA Strausberg R.;  
 RL Submitted (Feb-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC022256; AAH22256.1; -  
 DR GO; GO:0008289; F:lipid binding; IEA.  
 DR InterPro; IPR001124; LBP BPI CETP.  
 DR Pfam; PF01273; LBP BPI CETP\_1.  
 DR Pfam; PF02886; LBP BPI CETP\_C; 1.  
 DR SMART; SM00328; BPI1; 1.  
 DR SMART; SM00329; BPI2; 1.  
 DR PROSITE; PS00400; LBP BPI CETP; 1.  
 SQ SEQUENCE 477 AA; 52933 MW; 03D5E9D55A3BA6D0 CRC64;

Query Match 11.2%; Score 253; DB 4; Length 477;  
 Best Local Similarity 25.1%; Pred. No. 1.3e-10;  
 Matches 117; Conservative 83; Mismatches 195; Indels 72; Gaps 23;

QY 9 ILLALLL---PVVGASTPGTGVRLNKAALSYVSEIGKAPLQ-RALQVTVPHFELDSGEAL 64  
 DB 11 ILLALLLSTPEALGANFGLVARI-TKGLQYAAQSGLLALQSELLRLITLP---DFTGDLR 67  
 QY 65 QP-----TRIRILNVH-VRHLH--LKFIAGFGVRLAA-----ANFTKVPRAPELE- 109  
 DB 68 IPHVGRGRYEPHSLNTHSCHELLHSLRPVPGQGLSLISDSIRVQGRWKVRKSFKLQ 127  
 QY 110 -----LTLPEVLLADTRVQSSIRTPVVISACSLFSGHAN-EFDCSNSTSHALLVL 160  
 DB 128 SPDSVSKG-SISVNLGLG---SESSGR-FTVTASSCS--SDIADVEDVDSGELGWLNL 181  
 QY 161 ---VQKHKAVLSNKLCLISNLVQGVNVHLGTGLGNFVGPESQIRYSMVSVPTVTS 216  
 DB 182 HNQIESKQKVLSEKICEMIQKSVSDQLQYLQTLPTVTEIDSFADISLVEAPRATAQ 241  
 QY 217 YTSLEVNAPL-----LLGKPIILPTDTPFVLRHVGTEGSMATVGLSQQLFDSA 267  
 DB 242 MLEVMFKGEIFHRNHRSPVTLAAVMSLPEE-----HNQVYFAISDYVFNFA 289  
 QY 268 ILLQKAGALNDIT-GOLRSDN--LNTSALGRLIPEVARQPEPMPVVLKVLGATPV 325  
 DB 290 SWYHEBGLNFIISDMDIPDSNIRLTKTSRFPVRLARLYPN-MNLELQ---GSVPS 345  
 QY 326 A-XLHTNNATRLQPFVEV--LATASNSAFQSLFSDVVVNLRLQLSKVKLQGTTSVL 382  
 DB 346 AELLNFSNGLSVDPVMEIDAFVLLPSSSKPEVRLSVATNVSATLTENTSKITGLKP- 404  
 QY 383 GQVQLTVASSNVGFDITDQVRLMGTVFEKPLLDHLLNALLANGIALP 429  
 DB 405 GKVKVELKESKVLGNFNAELLEALLNYILNTFPKFNDKLAEGFPLP 451

RESULT 10  
 Q95JG0 PRELIMINARY; PRT; 503 AA.  
 AC Q95JG0;  
 DT 01-DEC-2001 (Tremblrel. 19, Created)  
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
 DE Phospholipid transfer protein.  
 GN PLTP.  
 OS Oryctolagus cuniculus (Rabbit).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 CX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Testis;  
 RA Masson D.; Lagrost L.; Bon P.;  
 RT "Oryctolagus cuniculus phospholipid transfer protein (PLTP) mRNA."  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AF382033; AAK69755.1; -.
DR GO; GO:0008289; F:lipid binding; IEA.
DR InterPro; IPR001124; LBP_BPI_CETP.
DR Pfam; PF01273; LBP_BPI_CETP; 1.
DR Pfam; PF02886; LBP_BPI_CETP_C; 1.
DR SMART; SM00328; BPI1; 1.
DR SMART; SM00329; BPI2; 1.
DR DR
DR PROSITE; PS00400; LBP_BPI_CETP; 1.
DR SEQUENCE 503 AA; 55582 MW; 963F49D6DE5E7D CRC64;

Query Match          7.9%; Score 179.5; DB 6; Length 503;
Best Local Similarity 20.9%; Pred.No.4.5e-05;
Matches 106; Conservative 88; Mismatches 208; Indels 105; Gaps 20;

QY      8  GLLALLPVPVGASTPGTVTVRLNKAALSYSEIGKAPLQRALQ-VTVPHFLDWSGEALQP 66
DB      5  GAVFLALLAGAHAEIPGCKRVITSEALNALVKQEGRLFELOEALAITPIDLRGEGHYF-- 62
QY      67  TRIRLNHVPRHLKFIAGVGVRLLAAANFTFKVFRAPPELEITLPVELL----- 117
DB      63  --YNISDKVTELQL---TGSELHFQPEQE--ALQITNA--SLGLRFRQLLYWFFYDGY 115
QY      118  ADRTVTOSS-RTPPVVISACSLFSGHANEEFGSN-----STSHA-----LL 158
DB      116  INASAEGVSR-T-----ALQSQSPAGOMEVSNVSCLASVSRMHAAPGCTFRKYVFLS 169
QY      159  VLQKHKKAVLSNKLK-----LSTSNLVQGVNVH--LCTLGLNPVGPDSEQRYRSMV 208
DB      170  TETTSGNRFLNLQICPVLHAGVNLNSLDTVPVRSANDELVID-----YSL 220
QY      209  SVPTVTSQSYSLSENAVILFL--GKPIILPTDPTFVLPRHVHTEGSMATVGLSQQLPDS 266
DB      221  KDPVVSNSYLTMEERGAFFPLAEGNSFLNAVEP-----QLQSEERMYVAFSEFFPDS 275
QY      267  ALLLLQKAGALNLDITG-QLRSD--DNLINTSALGRLI--PEVARQPPPEMPVVLKVRIG 321
DB      276  AMESYFRAGHLKLSGVGDKVPHDLIDLLRATYFSGIVLLSPAVI-----DSPKLKELQVT 330
QY      322  ATPVAMLHTNNATLR-----LQPEVEVLATASNAFOSLFLSDVVNVLRLQLS 369
DB      331  APPRCTIKESGTTISVTATVTIALVPMPQPEVQLSSVMVDARFSAKMALRGKA-LRTQLD 389
QY      370  VSKYKLOGT--SVLGDVQLTVASSNVGFDITDQVRLMGTVTEKPLDLHNALLANGIALP 429
DB      390  LRKERTYSNQAIESLAUI-----PLOAPLTLTLQIGVPMPLNERTWGVQIP 437
QY      430  GAVNLHYVAEPIFYEGYVWISSGLFY 456
DB      438  LPEGNEFREVWVTHAGFLTIGADLHF 464

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RESULT 11
Q8MWQ5
ID ID Q8MWQ5 PRELIMINARY; PRT; 503 AA.
AC Q8MWQ5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE phospholipid transfer protein.
DE PLTP.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI TaxID=9986;
[1]
RN
RP SEQUENCE FROM N.A.
RA Gander R., Eller P., Kaser S., Theurl I., Walter D., Sauper T.,
RA Ritsch A., Ratsch J.R., Foger B.;
RT "Molecular characterization of rabbit PLTP.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DDbj databases.
EMBL; AY072719; AAL66863.1; -
GC GO:0008289; F:lipid binding; IEA.
DR InterPro; IPR01124; LBP_BPI_CSTP.

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DR Pfam: PF01273; LBP_BPI_CETP; 1.
DR Pfam: PF02866; LBP_BPI_CETP_C; 1.
DR SMART: SM00328; BPI1; 1.
DR SMART: SM00329; BPI2; 1.
DR SMART: SM00329; BPI2; 1.
DR PROSITE: PS00400; LBP_BPI_CETP; 1.
DR SEQUENCE 503 AA; 55600 MW; 850995A71B1E8F38 CRC64;

Query Match 7.9%; Score 179.5; DB 6; Length 503;
Best Local Similarity 20.9%; Pred.No.4.5e-05;
Matches 106; Conservative 88; Mismatches 208; Indels 105; Gaps 20;

QY 8 GLILALLPVGCASTPGTVVRNKAISVYSBIGKAPLQALQ-VTVPHFLDWSGALQP 66
DB 5 GAVPLALLAGAAHEIPGCKIRVTSEALAVKQEGFLFQELEAIIPIRLRGREGHFY-- 62

QY 67 TRIRILNVHPRHLKFIAGFGVRLLAANFTKVFRAPEPELELTPEVLL----- 117
DB 63 --YNISDVKVTLEQL---TGSSELHFQPEQLALQITNA---SLGLRFRQLLYWFFYDGGY 115

QY 118 ADTRVTQSSIRTPWVSISACSLFSGHANFDDGSN-----STSHA-----LL 158
DB 116 INASAEVGSIRT-----ALQLSQGPAGQMRVSNVSCLASVSRMHAAGCTPRKVYEFLLS 169

QY 159 VLVQKHKEIKAVLSNKLC-----LSISNLVQGVNVH--LGTTLGNPNVPESQIRYSMW 208
DB 170 TPTSGMRFLNIQICPVYHAGMVLNLSLLOITVPVRSADVELVGLD-----YSLL 220

QY 209 SVETVTSYDISLEWNAVLELL--GKPIILPTDATTPLPRHVGTGCSMATVGLSQQLFDS 266
DB 221 KDPWVSNSYLDMEFRGAFFPLAEGNSWFLNRAVEP-----QLQEEBRMYVVAESEFFDSS 275

QY 267 ALLLQKAGALNDITG-QLRSD-DNLNLTSAIGRLI---PEVARQPEPEMPVVLKVRLLG 321
DB 276 AMESYFRAGALKLSLVGDQVPHLLDILLRATYGSIVLLSPAVI-----DSPKLKLEQVT 330

QY 322 ATPVAMLHTNNATLR-----LQPFVEVLATASNAPQSFLSDVVVNLRLQLS 369
DB 331 APPRCTIKPSGTTISVTATVTIALVPPMQPEVQLSSWMDARPSAKVALRGKA-LRTQLD 389

QY 370 VSKVKLGQITSVLGVQLTVASSNVGFDITDQVRLTNGTVFEKPELDHLNALLAMGIALP 429
DB 390 LRFRMYNSQASLESALII-----PLQAFILKILLQIGVPMPLNERTWRGVQIIP 437

QY 430 GVVNLHYVAPEIFVYEGYVVISGLFY 456
DB 438 LPGICNFVREVVTNHAGFLITIGADLHF 464

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RESULT 12
Q8WNW7
ID Q8WNW7 PRELIMINARY; PRT; 496 AA.
AC Q8WNW7;
DT 01-MAR-2002 (T-EMBLrel. 20, Created)
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Plasma phospholipid transfer protein.
GN PLTP.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
R3 SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=97396085;
RA Pussinen P.J., Oikkonen V.M., Jauhainen M., Ehnholm C.;
RT "Molecular cloning and functional expression of cDNA encoding the pig
RT plasma phospholipid transfer protein.";
EL J. Lipid Res. 38:1473-1481(1997).
DR ENBL; L78843; AAL40162.1; -.
DR GC; GO:0008289; Filipid binding; TEA.
DR InterPro; IPR001124; LBP_BPI_CETP.
DR Pfam; PF01273; LBP_BPI_CETP; 1.

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DR Pfam; PF02886; LBP\_BPI\_CETP\_C; 1.

DR SMART; SM00328; BPI1; 1.

DR SMART; SM00329; BPI2; 1.

DR PROSITE; PS00400; LBP\_BPI\_CETP; 1.

SQ SEQUENCE 496 AA; 54922 MW; ECID02CB1493A88 CRC64;

Query Match 7.4%; Score 166.5; DB 6; Length 496;

Best Local Similarity 21.0%; Pred. No. 0.0041;

Matches 107; Conservative 94; Mismatches 201; Indels 107; Gaps 21;

7 LGLLALLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQALQ-VTVP-----HP-- 56

4 LGALFLVLGAAHAEPLQCKIRITSKALELVKQEGLEFLEQLETTITPDLRGREGHFY 63

57 -----LDWSEGLQPTRIILNVHVRHLKF-----IAGF-----GVRLAAANFT 98

64 NISEVKVTELGTSSELHFQPEQLMLQINGSLGRFRQLLYWFFDGGYINASA--- 120

99 PKVFRAPPELETLFVELLAD-----TRVQSGIRTPVVSISACSLFSG---HANFEDGSN 151

121 -----EGVSIHTALQSLSDPTGRIKVSNVSCQASVSRMHA--FGGTEKKVYEFLE 171

152 STSHALLVQKHIAVLNKLCLISINLVQGVNH--LGLTGLNLPVPSQIRYSNWS 209

172 ITS-GMRELLNQOICPVLYHAGWVJNSLSDTPVVRGAVDELVGID-----YSLK 221

210 VPTVTSYISLEVNVAFLGKPIILPTDA-PFVLPF-----HVGTEGSMATVGLSQQLF 264

222 DPVASTSNLMEFRGAFY-----PLAEGNWSLPNRRVFPQLQEEEMVYVAESEFF 273

265 DSALLLQKAGALNLDITG-QLRSD-DNLMTSALGRLLI---PEVAROPPEPMPVLKVR 319

274 DSAMESYFRAGALKSLVGVDPHDLMLLRATYFGSIW-LSPAVI-----DSPKLLELR 328

320 LGATPVAMLHTNATLRL-----QPFVEVLATANSAPQSLFSLDVVNLRLQ 367

329 VMAFPRTCTIKPSGTISVTSVTLVPPGPEVQLSMTDRLSAAKMLRGKA-LRTQ 387

368 LSVSKVKLOGTTSLVGLDQVLTAVASSNVGFDIDQVRLMGVTFEKLPLDLNALLAMGIA 427

388 LQLRERFYSQSALESALI-----PLQAPLKTMLQIGVMPMLNERTWRGVQ 435

428 LPGVNHLHYVAPEIFVVEGYVVISGLFY 456

436 IPLEEGINFVREVVTNNAGFLTIGADLHF 464

RESULT 13

ID Q81729

AC Q81729

DT 01-MAR-2003 (TRENBLrel. 23, Created)

DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)

DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)

DE LBP/BPI.

OS Crassostrea gigas (Pacific oyster).

OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pterio-cipha; Ostreoida;

OC Ostreoida; Ostreidae; Crassostrea.

OX NCBI\_TaxID=29159;

RN [1]

RP SEQUENCE FROM N.A.

RA Gonzalez M., Bacher E., Escoubas J.M., Guguen Y.;

RA "Crassostrea gigas LBP (LPS binding-protein)/BPI

RT (bactericidal/permeability-increasing protein) mRNA."

RL Submitted (OCT-2002) to the EMBL/GenBank/DBAJ databases.

DR EMBL; AY165040; AAN4552.1; -

DR GO; GO:0008289; F:lipid binding; IEA.

DR InterPro; IPR001124; LBP\_BPI\_CETP.

DR Pfam; PF01273; LBP\_BPI\_CETP; 1.

DR Pfam; PF02886; LBP\_BPI\_CETP\_C; 1.

DR SMART; SM00328; BPI1; 1.

DR SMART; SM00329; BPI2; 1.

SQ SEQUENCE 477 AA; 52192 MW; 928BF7FC293DB7B1 CRC64;

Query Match

Best Local Similarity 20.3%; Pred. No. 0.004;

Matches 103; Conservative 88; Mismatches 216; Indels 100; Gaps 23;

10 LLALLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQALQVTVPHFLDWSGEA---LQ 65

9 VVSLFVTSQAQCKTPGLQTRITDRALAYATEVALDILSK--QVTGQQIPDQHGSGDVKFD 66

66 PTRIRILNVHVRHLKFTIAGFGRV-----LLAANFTFKVFA-----P 105

67 ITGMNVKQFTKSSRVSLIQNVLSWSTGTGLAHGDFKYKRYKGIKISDHGSDFLKA 126

106 EPLELTLPVEILADTRVQSSIRTPVVSISACSLFSGHAN-EFDGNSNSTSHALLVLVQKH 164

127 NGINFOIKIEIGMD-----GTGRPTMKAVGSCNVGSADIKFHGGAWIYNL----- 173

165 IKAVLSNKLCLISINLVQGVN---VHLGTLGLN-----PVGPESQIR---YSMW 208

174 FSGQLENKL---XDMVGGGGLLCKQLNTLIDVNGMKSLOKLPTVTVQAKRFLDYRFL 229

209 SVPTVTSYISL---EV--NAVLELLGKPIILPTDAPFVLPVRHVGTSGS--YATVGLS 260

230 SKPSPQTKFPMETHYKGEVYVNAV-----PVDA-PFAAPPLDKSSDTRMMYIWS 278

261 QOLFDSALLLQKAGALNLDITGQLRSDNLLNT-----SALGRLLIPEVAROPPEMPVV 315

279 DYVNTMSYNALKYINQLOVYNTK-DLPSGLVNTTTPQSTCGIKIKAIGTRFPN-TTV 336

316 LKVRIGATPVAMLHTNATLRLQPFVEVLATANSAPQSLFSLDVVNLRLQSLV----- 370

337 LYMKSTSPENMTAQMGSTVWNASGDIVFFAQPGGKYTYFLTSATMTTISIMIENEKV 396

371 -SKVLQGTTSVLGDPQLTVASSNVGFDIDQVRLMGVTFEKLPLDLNALLAMGIALP 429

387 FAKVLKLPISVTVKSDKIPVSPBGLNFI---VKGIV-SVFVEP---KUNELGAAGFPLP 448

430 GVVNHLHYVAPEIFVVEGYVVISGLFY 456

449 VINSVHTNTQITVAKOTLLATLTKY 475

RESULT 14

ID Q8VVC2

AC Q8VVC2

DT 01-MAR-2002 (TRENBLrel. 20, Created)

DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)

DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)

DE Putative bactericidal permeability-increasing protein.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosids 11; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI\_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RA Yamada K., Bach J., Chan M.M., Chang C.H., Chang E., Dale J.M.,

RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,

RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,

RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,

RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,

RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,

RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.,

RA Davis R.W., Ecker J.R., Theologis A.;

RT "Full length cDNA of gene At3g20270 (GI:15231086).";

RL Submitted (JAN-2002) to the EMBL/GenBank/DBAJ databases.

DR EMBL; AY072195; AAL60017.1; -

DR GO; GO:0008289; F:lipid binding; IEA.

DR InterPro; IPR001124; LBP\_BPI\_CETP.

DR Pfam; PF01273; LBP\_BPI\_CETP; 1.

DR Pfam; PF02886; LBP\_BPI\_CETP\_C; 1.

DR SMART; SM00328; BPI1; 1.

DR SMART; SM00329; BPI2; 1.

SQ SEQUENCE 477 AA; 52192 MW; 928BF7FC293DB7B1 CRC64;

DR SMART; SM00328; BPI1; 1.  
DR SMART; SM00329; BPI2; 1.  
SQ SEQUENCE 515 AA; 5671

Query Match 6.5%; Score 147.5; DB 10; Length 515;  
Best Local Similarity 17.7%; Pred. No. 0.012;  
Matches 82; Conservative 108; Mismatches 216; Indels 57;

Query Match	6.5%;	Score 147.5;	DB 10;	Length 515;
Best Local Similarity	17.7%;	Pred. No. 0.012;		
Matches	82;	Conservative 108;	Mismatches 216;	Indels 57; Gaps 16;
QY	7	LGILLALLLPVGASTPQTWRINKAA--LSYVSEIG-----KAPLORALQVTPPHFL-D 58		
Db	39	YALMKVMTILVLFVSVSITLAQSNNGGHSIIIVSETGLEPAKDYLIKXVITTLPLQLPD 98		
QY	59	WSEALQP-----TIRILNVHVPRLHK-----FIAGFVRLIAAANPFKV 101		
Db	99	IENKVKFLIGKVMGSLNSIQIDAVHVQSSKMETKDGIIILSVLGATANLSMOWSYTYRA 158		
QY	102	--FRAPPELELTLPVELLADPTVQSSIRTPVWSISACSLFSGHANFDFGNSNSTSH---- 155		
Db	159	SFFEISDHGQASVEVKGM-NVRIIAT-----LVNDGSLKIASRENDCTVKNIIDHNGG 212		
QY	156	-----ALLVLVQGHKAVLSENKCLISNLVQGVNVHLGTILGNLPVGPESQTRYSMVS 209		
Db	213	ASWLYQGWDFAQKMIILSTVEKTYSTKIIEKMKKLDSFLQSLPKQRKIDDDSAAVNLFTG 272		
QY	210	VPTVTSYVISLEVNAMVFLFLCKPI-ILPTDATPFVLPRHVGTGECSMATVGLSQQLFQSA 268		
Db	273	NPVLGNSSEVVDINGLFWPKGDDIKVAGSRSSF-----FGWNKRMVTIISVEGVENSAT 328		
QY	269	LLQKAGALNLDITQGLRSDNLLNTSALGRLIPEVAQPEPMPVVLKVLGATPTVAML 328		
Db	329	LVYFNKVMHLVM--EETKNGSILSTSDWKLLILPELYKHYED-NKMVLNMGVTSPPAVKI 385		
QY	329	HTN--NATLRQPFEVLATASNAFQSLFLCVVNVNLRLLQLSYSKVKLCQTTSVLGDPVQ 386		
Db	386	TENGIDATIQICLIAFDVQDSGEN---LSVARLSITLIVACSTEIVKKNLIGSLR-LNDFN 441		
QY	387	LTVASSNVGFIDTQVTRLMGTVFTEKPLLDHNLALLAMGIALP 429		
Db	442	ATMKWSKIGEFOTNVVOATSRILEALPLPVNTRLRKGFPLP 484		

RESULT 15

Q93796 PRELIMINARY; PRT; 551 AA.  
AC Q93796;  
AD Q93796;  
DT 01-FEB-1997 (TREMBLrel. 02, Created)  
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Hypothetical protein F55B12.5.  
DE F55B12.5  
GN F55B12.5  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdiida; Rhabditoidea;  
OC Rhabditidae; Pterodermidae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sims M.A.;  
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99069613; PubMed=9851916;  
RA none;  
RT "Genome sequence of the nematode C.elegans: A platform for  
RT investigating biology.";  
RL Science 282:2012-2018 (1998).  
DR EMBL; Z79757; CAB02126.2; -  
DR PIR; T22700; T22700.  
DR WormPep; F55B12.5; CE32438.  
DR GO; GO:0008289; Lipid binding; IEA.  
DR InterPro; IPR001124; LBP\_BPI\_CEP.  
DR SMART; SM00328; BPI1; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 551 AA; 60850 MW; D4FE291494D27680 CRC64

Query Match	5.7%;	Score 129;	DB 5;	Length 551;	
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Db	32	GIYVRLNQKAVDVYADLASDALPAILNLSPF--DIVTDMAKITKLHISNVAKENLSAKF	89		
		: : : : :			
Qy	84	IAGFVGLLAAANFTKVPFAPFPLELTVP-----ELLADTFTVQSSIRTPV	131		
		: : : : :			
Db	90	IDDKGV---AYANISLASFASAYAEISVFWVSYEGDFTABLRELSFESSELPFDYNGTTT	145		
		: : : : :			
Qy	132	VSIISACSLFSGHANFPGSNSTSHALLVLVQKHKAVLSNKLCLISISNLVQGVNVHIGTL	191		
		: : : : :			
Db	146	VNASVCNVTHSELSELPFGPGSSLALQSEIKGQIVSALRDVAVC--FTAVEA---LTFV	198		
		: : : : :			
Qy	192	IGLNPVGPS-----QIRYSWVSVFTVT--SDYISLVNVAVLFLIGKP	232		
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Db	199	MAQKPIEPSEPNYQKPEAGDPNGFVSVAELGASLCQVDVTNMGFDSQEBQGNVETVATPT	258		
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Qy	233	-----IILPTDAPVLPVRHVGTEGSM-----ATVGLSQOLFSAIIL--LQKAGA	276		
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Qy	323	TPVAMLHTN-NATLRLQPFVEV-----LATASNAFQSLFSLDVMNLRQLSVSK	372		
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Search completed: June 29, 2004, 11:00:22  
Job time : 48 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 29, 2004, 20:34:40 ; Search time 11448 seconds  
(without alignments)  
6932.311 Million cell updates/sec

Title: US-10-069-034-65

Perfect score: 1831

Sequence: 1 gctc-taataagtagcctctg.....ttgagtgcaaaaaaaaaa 1831

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 216715:6995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBank:

1: gb.ba.\*  
2: gb.htg.\*  
3: gb.in.\*  
4: gb.om.\*  
5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pl.\*  
9: gb.pr.\*  
10: gb.ro.\*  
11: gb.sts.\*  
12: gb.sy.\*  
13: gb.un.\*  
14: gb.vi.\*  
15: em.ba.\*  
16: em.fun.\*  
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19: em.mu.\*  
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41: em.htgo.other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1831	100.0	1831	6	AX083523 Sequence
2	1816.8	99.2	1820	5	AX376430 Sequence
3	1816.8	99.2	1820	5	AX454736 Sequence
4	1816.8	99.2	1820	6	AX491214 Sequence
5	1816.8	99.2	1820	9	AX358723 Homo sapi
6	1810.4	98.9	1812	6	AX280153 Sequence
7	1810.4	98.9	1928	9	AK027068 Homo sapi
8	1773.8	96.9	1794	6	AX166348 Sequence
9	1772.2	96.8	1794	6	AX166346 Sequence
10	1764.2	96.4	1842	9	BC034415 Homo sapi
11	1375.4	75.1	1377	9	AF465765 Homo sapi
12	1374	75.0	1374	6	AX166357 Sequence
13	1372.4	75.0	1374	6	AX166356 Sequence
14	1076.4	58.8	1533	6	AX380531 Sequence
15	367	20.0	129502	9	HSDJ726C3
16	123.2	6.7	255562	2	AC095199
17	123.2	6.7	298126	2	AC128629
18	120.4	6.6	168210	2	AC116700
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20	107.8	5.9	1842	6	AX283507 Sequence
21	107.8	5.9	1914	6	AX283509 Sequence
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28	92	5.0	1733	10	RRYA3
29	89.6	4.9	1597	5	AF029841 Gallus ga
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38	67.4	3.7	1741	5	AB042026 Oncorhync
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43	65	3.5	125020	9	AF429315 Homo sapi
44	61.8	3.4	7218	6	I66494 Sequence 14
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# ALIGNMENTS

RESULT 1	AX083523	Sequence 65 from Patent WO0112662.	1831 bp	DNA	linear	PAT 28-FEB-2001
LOCUS	AX083523	Sequence 65 from Patent WO0112662.	1831 bp	DNA	linear	PAT 28-FEB-2001
DEFINITION	AX083523	Sequence 65 from Patent WO0112662.	1831 bp	DNA	linear	PAT 28-FEB-2001
ACCSSION	AX083523	Sequence 65 from Patent WO0112662.	1831 bp	DNA	linear	PAT 28-FEB-2001
VERSION	AX083523.1	GI:13185333	1831 bp	DNA	linear	PAT 28-FEB-2001
KEYWORDS	AX083523.1	GI:13185333	1831 bp	DNA	linear	PAT 28-FEB-2001
SOURCE	AX083523.1	GI:13185333	1831 bp	DNA	linear	PAT 28-FEB-2001
ORGANISM	AX083523.1	GI:13185333	1831 bp	DNA	linear	PAT 28-FEB-2001
REFERENCE	AX083523.1	GI:13185333	1831 bp	DNA	linear	PAT 28-FEB-2001
AUTHORS	AX083523.1	GI:13185333	1831 bp	DNA	linear	PAT 28-FEB-2001
TITLE	AX083523.1	GI:13185333	1831 bp	DNA	linear	PAT 28-FEB-2001

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa;

Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates;

Catarrhini; Homidae; Homo.

1

Lal, P., Yue, H., Tang, Y. T., Bandman, O., Burford, N., Aizmai, Y.,

Baughn, M. K., Lu, D. A. and Patterson, C.

Membrane associated proteins





SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Baker, K.P., Chen, J., Desnoyers, L., Goddard, A., Godowski, P.J.,  
Gurney, A.L., Pan, J., Smith, V., Watanabe, C.K., Wood, W.I. and  
Zhang, Z.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
JOURNAL Patent: WO 0168848-A 497 20-SEP-2001;  
Genentech, Inc. (US)  
FEATURES Location/Qualifiers  
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/db\_xref="taxon:9606"  
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Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1818; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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DB 1 GCCTTATAAGTAGCTCTGCATCTGCTGCTCGGCGAGAGGGGTACCCCTGGGGCT 60  
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DB 61 GAGAGTTACCTGTCACGAAACACCTGAGCCACAGATCTGTGCGAGCGGCCAGGG 120  
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QY 1801 AACAACTTCTCTGAGCTGC 1820  
DB 1801 AACAACTTCTCTGAGCTGC 1820



















REFERENCE	ORIGIN
1 Mammalia, Eutheria; Primates; Catarrhini; Hominoidea; Homo.	
1 Ballinger,D.G., Mulero,J.J., Qian,X., Mize,N.K., Halsey,D.A. and Boy'e,B.J.	
TITLE Methods and compositions relating to bactericidal/permeability increasing factor-like polypeptides and polynucleotides	
JOURNAL Patent: WO 0136478-A 1 25-MAY-2001;	
HYSEQ, INC. (US)	
FEATURES	
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1787	QY	GCCTCTTGTCATTAAACAACACTCTCTCTGAGCTGCAAAAAA	1831
1741	Db	GCCTCTTGTCATTAAACAACACTCTCTGAGCTGCAACTTCAAA	1785
<p>BC034415 1842 bp mRNA linear PRI 12-NOV-2003</p> <p>Homo sapiens bactericidal/permeability-increasing protein-like 1,</p> <p>mRNA (cDNA clone MGC:34059 IMAGE:5173032), complete cds.</p> <p>BC034415 GI:21706775</p> <p>MGC.</p> <p>Homo sapiens (human)</p> <p>Homo sapiens</p> <p>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;</p> <p>Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.</p> <p>1 (bases 1 to 1842)</p> <p>Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,</p> <p>Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,</p> <p>Altshul,S.F., Zerborg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,</p> <p>Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,</p> <p>Diatchenko,L., Marusina,K., Farmer,A., Rubin,G.M., Hong,L.,</p> <p>Scapetot,M., Soares,M.B., Bonaldo,M.P., Casavant,T.L.,</p> <p>Chabot,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,</p> <p>Carinci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,</p> <p>Aranson,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J.,</p> <p>McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,</p> <p>Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Eulyk,S.W.,</p> <p>Villaion,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,</p> <p>Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,</p> <p>Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,</p> <p>Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,</p> <p>Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,</p> <p>Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,</p> <p>Scherch,A., Schein,J.E., Jones,S.J. and Marra,M.A.</p> <p>Generation and initial analysis of more than 15,000 full-length</p> <p>human and mouse cDNA sequences</p> <p>Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)</p> <p>22388257</p> <p>2 (bases 1 to 1842)</p> <p>Strausberg,R.</p> <p>Direct Submission</p> <p>Submitted (02-JUL-2002) National Institutes of Health, Mammalian</p> <p>Gene Collection (MGC), Cancer Genomics Office, National Cancer</p> <p>Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,</p> <p>USA</p> <p>NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a></p> <p>Web site: <a href="http://www.hgsc.bcm.tmc.edu/cdna/">http://www.hgsc.bcm.tmc.edu/cdna/</a></p> <p>Contact: <a href="mailto:amgobcm.tmc.edu">amgobcm.tmc.edu</a></p> <p>Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Lounseged, H.,</p> <p>Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,</p> <p>A.N., Gibbs, R.A.</p> <p>Clone distribution: MGC clone distribution information can be found</p> <p>through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a></p> <p>Series: IRAC Plate: 51 Row: J Column: 24</p> <p>This clone was selected for full length sequencing because it</p> <p>passed the following selection criteria: matched mRNA gi: 15055534</p> <p>Location/Qualifiers</p>			
RESULT 10			
BC034415			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REMARK			
COMMENT			
FEATURES			

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## RESULT 11

AP465765

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

gene

CDS

ORIGIN

Query Match

Best Local Similarity

Matches 1376; Conservative

75.1%; Score 1375.4; DB 9; Length 1377;

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1377 bp mRNA linear PRI 02-JUL-2002  
 Homo sapiens bactericidal/permeability-increasing protein-like 1  
 (BPI1) mRNA, complete cds.

AP465765  
 AP465765.1 GI:21667209

Homo sapiens (human)  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1377)  
 Mulero, J.J., Boyle, B.J., Bradley, S., Bright, J.M., Nelken, S.T.,  
 Ho, T.T., Mize, N.K., Childs, J.D., Ballinger, D.G., Ford, J.E. and  
 Rupp, F.

Three new human members of the lipid transfer/lipopolysaccharide  
 binding protein family (LT/LBP)  
 Immunogenetics (2002) In press

2 (bases 1 to 1377)  
 Mulero, J.J., Boyle, B.J., Bradley, S., Bright, J.M., Nelken, S.T.,  
 Ho, T.T., Mize, N.K., Childs, J.D., Ballinger, D.G., Ford, J.E. and  
 Rupp, F.

Direct Submission  
 Submitted (07-JAN-2002) Functional Genomics, Hyseq Pharmaceuticals,  
 675 Almanor Ave., Sunnyvale, CA 94085, USA

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ORIGIN  
 Query Match 75.1%; Score 1375.4; DB 9; Length 1377;  
 Best Local Similarity 99.9%; Pred. No. 1.8e-285;  
 Matches 1376; Conservative 0; Mismatches 1; Indels 0; Gaps 0;















GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OX nucleic - nucleic search, using sw model

Run on: June 25, 2004, 20:33:10 ; Search time 1059 Seconds

(without alignments)  
7345.090 Million cell updates/sec

Title: US-10-069-034-65

Perfect score: 1831

Sequence: 1 gccctataagtagcctctg.....ttgagctgcaaaaaaaaaa 1831

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq 29Jan04:\*

1: Geneseq1980s:\*

2: Geneseq1990s:\*

3: Geneseq2000s:\*

4: Geneseq2001as:\*

5: Geneseq2001bs:\*

6: Geneseq2002s:\*

7: Geneseq2003as:\*

8: Geneseq2003bs:\*

9: Geneseq2003cs:\*

10: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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4	1816.8	99.2	1820	6	Ab195721 Human ang
5	1816.8	99.2	1820	7	Abx78776 Human PRO
6	1816.8	99.2	1820	7	Aca75748 Novel hum
7	1816.8	99.2	1820	7	ACA71228 Human sec
8	1816.8	99.2	1820	7	Acc87756 Human sec
9	1816.8	99.2	1820	7	Acc87142 Human sec
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37	1816.8	99.2	1820	7	ACD08397	ACD08397 Human sec
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## ALIGNMENTS

## RESULT 1

Aaf81768

ID Aaf81768 standard; cDNA; 1831 BP.

XX AC Aaf81768;

XX DT 12-JUN-2001 (first entry)

XX DE Human membrane associated protein MEMAP-28 encoding cDNA.

XX KW Human; membrane associated protein; MEMAP; diagnosis; cytostatic;

XX KW antiinflammatory; anticonvulsant; immunosuppressive; antidiarrhetic;

XX KW antiarteriosclerotic; gene therapy; cell proliferative disorder;

XX KW autoimmune disorder; inflammatory disorder; neurological disorder;

XX KW gastrointestinal disorder; cancer; inflammation; atherosclerosis;

XX KW epilepsy; diarrhoea; ss.

XX OS Hmo sapiens.

XX PN WC200112662-A2.

XX PD 22-FEB-2001.

XX PF 14-AUG-2000; 2000WO-US022315.

XX PR 17-AUG-1999; 99US-0149641P.

XX PR 09-NOV-1999; 99US-0164203P.

XX PA (INCY-) INCYTE GENOMICS INC.

XX PI Lal P, Yue H, Tang YT, Bandman O, Burford N, Azimzai Y;

XX PI Baughn MR, Lu DAM, Patterson C;

XX DR WPI; 2001-168860/17.

XX DR P-PSDB; AAB74722.

XX PT Isolated polypeptide with a human membrane associated protein sequence is

XX PT useful for the diagnosis, prevention and treatment of cell proliferative,

XX PT autoimmune/inflammatory, neurological and gastrointestinal disorders.

XX PS Claim 5; Page 167; 173pp; English.

XX CC AAF81741 to AAF81777 encode the human membrane associated proteins

XX CC (MEMAP) given in AAB74695 to AAB74731. MEMAPs have cytostatic,

XX CC antiinflammatory, anticonvulsant, immunosuppressive, antidiarrhetic and

XX CC antiarteriosclerotic activities, which can be used in gene therapy.





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XX vulnerable; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;  
XX gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
XX angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
XX age-related macular degeneration; arterial restenosis; angina;  
XX rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
XX lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
XX wound healing; chromosome mapping; gene mapping; gene; ss.  
OS Homo sapiens.  
XX WO200200690-A2.  
XX 03-JAN-2002.  
XX 20-JUN-2001; 2001WO-US019692.  
XX 23-JUN-2000; 2000US-0213637P.  
XX 20-JUL-2000; 2000US-0219556P.  
XX 25-JUL-2000; 2000US-0220624P.  
XX 25-JUL-2000; 2000US-0220664P.  
XX 28-JUL-2000; 2000WO-US020710.  
XX 02-AUG-2000; 2000US-0222695P.  
XX 17-AUG-2000; 2000US-00643657.  
XX 23-AUG-2000; 2000WO-US023522.  
XX 24-AUG-2000; 2000WO-US023328.  
XX 07-SEP-2000; 2000US-0230978P.  
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XX 01-JUN-2001; 2001WO-US017800.















XX DE Kovel human secreted and transmembrane protein PRO5776 cDNA.  
XX KW Human; secreted and transmembrane protein; PRO; gene therapy;  
XX KM tumour necrosis factor-alpha release; TNF-alpha release;  
KW chondrocyte proliferation; chondrocyte differentiation; tumour;  
KW adrenal tumour; lung tumour; colon tumour; breast tumour;  
KW prostate tumour; rectal tumour; cervical tumour; liver tumour; gene; ss.  
XX OS Homo sapiens.  
XX XX  
XX PN US2003032127-A1.  
XX DD -3-FEB-2003.  
XX XX  
XX PF 26-JUN-2002; 2002US-00183012.  
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DT 02-AUG-2003 (first entry)
XX XX
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XX XX
KW Human; gene; ss; secreted and transmembrane protein; PRO; TNF-alpha;
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing.
XX XX
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PN US2003032112-A1.
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PD 13-FEB-2003.
XX XX
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## RESULT 9

ACC87142

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XX AC ACC87142;

DT 05-AUG-2003 (first entry)

XX 05-AUG-2003 (first entry)

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XX Human; PRO; secreted protein; transmembrane protein;

KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;

KW chondrocyte; proliferation; differentiation; cartilage disorder;

KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;

KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;

KW liver; drug screening; transgenic animal; genetic analysis;

KW antiarthritic; vulnery; gene therapy; gene; ss.

OS Homo sapiens.

XX Homo sapiens.

XX US2003036159-A1.

PN 20-FEB-2003.

XX 20-FEB-2003.

XX 02-JUL-2002; 2002US-00188773.

XX 18-SEP-1997; 97US-0059263P.

XX 18-SEP-1997; 97US-0059266P.

XX 17-OCT-1997; 97US-0062250P.

XX 21-OCT-1997; 97US-0063486P.

XX 24-OCT-1997; 97US-0063120P.

XX 24-OCT-1997; 97US-0063121P.

XX 28-OCT-1997; 97US-0063540P.



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QY 61	GAGAGTTTCACCTGTCTCAGGAACACACCTGAGCCCCACAGATCCTGTGGGACGGGCCAAGG	120		
DB 61	GAGAGTTTCACCTGTCTCAGGAACACACCTGAGCCCCACAGATCCTGTGGGACGGGCCAAGG	120		
QY 121	CAGCCATGGCTTGGGCAAGTAGGCTGGGCCCTGTCTGGCACTGCTGCTGCCCTGCCCTGGCTGGTGG	180		
DB 121	CAGCCATGGCTTGGGCAAGTAGGCTGGGCCCTGTCTGGCACTGCTGCTGCCCTGGCTGGTGG	180		
QY 181	GTGCCTCCACGCGAGGACCTGTGTCACCTCAACAAGGACGATTGAGTACGCTGCTG	240		
DB 181	GTGCCTCCACGCGAGGACCTGTGTCACCTCAACAAGGACGATTGAGTACGCTGCTG	240		
QY 241	AAATTGGAAAGCCCTCTCCAGCGGGCCCTGCAGGTCACTGTCCCTCATTTTCCTGGACT	300		
DB 241	AAATTGGAAAGCCCTCTCCAGCGGGCCCTGCAGGTCACTGTCCCTCATTTTCCTGGACT	300		
QY 301	GGAGTGGAGAGCGCTTCAGGCCACAGATCCGGATTCTGAATCTCCATGTCGCCCGCC	360		
DB 301	GGAGTGGAGAGCGCTTCAGGCCACAGATCCGGATTCTGAATCTCCATGTCGCCCGCC	360		
QY 361	TCCACCTGAAATTCATTGCTGGTTCGGAGTGGCGCTGTGGCAGCAGCTAATTTACTT	420		
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QY 421	TCAAGGTCTTTTCGCGCCCGCAGAGCCCTTGAGCTGACCGTGTGGAACTGCTGCTG	480		
DB 421	TCAAGGTCTTTTCGCGCCCGCAGAGCCCTTGAGCTGACCGTGTGGAACTGCTGCTG	480		
QY 481	ACACCGCGTGACCCAGAGTCTCATCAGGACCCCTGTGGTCAAGCATCTGCTGCTCTT	540		
DB 481	ACACCGCGTGACCCAGAGTCTCATCAGGACCCCTGTGGTCAAGCATCTGCTGCTCTT	540		
QY 541	TATTCCTGGGGCCACGCCAACGAGTTTGATGGCAGTAACAGCACTCCCAACGCGTGTG	600		
DB 541	TATTCCTGGGGCCACGCCAACGAGTTTGATGGCAGTAACAGCACTCCCAACGCGTGTG	600		
QY 601	TCTTGTTCAGAGCAGCATTAAGCTGCTTCAGTAAACAGCTGTGCTGAGCATCTCCA	660		
DB 601	TCTTGTTCAGAGCAGCATTAAGCTGCTTCAGTAAACAGCTGTGCTGAGCATCTCCA	660		
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			98US-0084366P
Qy	1801	AACAACTCTCTTGAGCTGC	98US-0084414P
			98US-0084639P
Db	1801	AACAACTCTCTTGAGCTGC	98US-0084640P
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			98US-0085579P
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			98US-0085582P
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XX			98US-0086486P
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XX			98US-0087759P
DE	Human secreted/transmembrane protein (PRO) cDNA #249.		98US-0087759P
XX			98US-0088272P
XX	Human; gene; ss; secreted and transmembrane protein; PRO; TNF-alpha;		98US-0088025P
KW	tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;		98US-0088028P
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Query Match 99.2%; Score 1816.8; DB 7; Length 1820;  
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Matches 1818; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db	61	GAGAGTTACCTGTCTCAGGAACCACTGAGCCACAGATCCTGTGGGAGCGGCCAGGG	120
Qy	121	CAGCCATGGCTTGGGCAAGTAGAGCTGGGCTGCTGCTGGCACTGCTGCTGCTGGCTG	180
Db	121	CAGCCATGGCTTGGGCAAGTAGAGCTGGGCTGCTGCTGGCACTGCTGCTGCTGGCTG	180
Qy	181	GTGCTTCCACCGCCAGGCAACGCTGGTCCGACTCAACAGGAGCAGATTGAGCTAGCTGT	240
Db	181	GTGCTTCCACCGCCAGGCAACGCTGGTCCGACTCAACAGGAGCAGATTGAGCTAGCTGT	240
Qy	241	AAATGGGAAAGCCCTCTCCAGGGGCCCTCAGAGTCACTGCTCCCTCATTTCTGGACT	300
Db	241	AAATGGGAAAGCCCTCTCCAGGGGCCCTCAGAGTCACTGCTCCCTCATTTCTGGACT	300
Qy	301	GGAGTGGAGAGGCGCTTCAGCCACAGGATCCGATTTCTGAATGTCCATGTGCCCCGCC	360
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Qy	361	TCCACCTGAAATTCATTTGCTGTTTGGAGTGGCCCTGCTGGCAGCAGCTAAATTTACTT	420
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Qy	421	TCAGGTCTTTTCGGGCCAGAGCCCTGAGCTGAGCTGCTGCTGCTGGAAGTGGTGGCTG	480
Db	421	TCAGGTCTTTTCGGGCCAGAGCCCTGAGCTGAGCTGCTGCTGCTGGAAGTGGTGGCTG	480
Qy	481	ACACCGCGTGACCCAGAGCTCCATCAGGACCCCTGCTGGTCAAGATCTCTGCTGCTCTT	540
Db	481	ACACCGCGTGACCCAGAGCTCCATCAGGACCCCTGCTGGTCAAGATCTCTGCTGCTCTT	540
Qy	541	TATTTCTGGGCCAGCCACAGTTTGTATGCGAGTAAACAGCACTCCACCGCGTGTGG	600
Db	541	TATTTCTGGGCCAGCCACAGTTTGTATGCGAGTAAACAGCACTCCACCGCGTGTGG	600
Qy	601	TCCTGTGAGAGACATTAAGCTCTTCTGAGTAAAGCTGCTGGCTGAGCAGCTCTCCA	660
Db	601	TCCTGTGAGAGACATTAAGCTCTTCTGAGTAAAGCTGCTGGCTGAGCAGCTCTCCA	660
Qy	661	ACCTGTGAGAGGTGCTCAATGTCACCTGGGCACTTAAATTTGGCTCAACCCCGTGGCTC	720
Db	661	ACCTGTGAGAGGTGCTCAATGTCACCTGGGCACTTAAATTTGGCTCAACCCCGTGGCTC	720
Qy	721	CTGAGTCCAGATCCGCTATTCCATGCTGAGTGGCCCACTGTCAACAGTCACTATT	780
Db	721	CTGAGTCCAGATCCGCTATTCCATGCTGAGTGGCCCACTGTCAACAGTCACTATT	780
Qy	781	CCCTGGAAGTCAATGCTGTTCTCTTCTGCTGGGCAAGCCCATCATCTGCTCCAGGATG	840
Db	781	CCCTGGAAGTCAATGCTGTTCTCTTCTGCTGGGCAAGCCCATCATCTGCTCCAGGATG	840
Qy	841	CCACCCCTTTGTTGTCGCAAGGATGTGGGTACCGAGGGCTCCATGGCCACCGTGGGCC	900
Db	841	CCACCCCTTTGTTGTCGCAAGGATGTGGGTACCGAGGGCTCCATGGCCACCGTGGGCC	900
Qy	901	TCTCCAGCAGCTGTTTGACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	960
Db	901	TCTCCAGCAGCTGTTTGACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	960
Qy	961	TGGACATCAGAGGAGCTGAGTGGATGATCAACCTGCTGCAACACCTCTGCTGCTGGGCC	1020
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Qy	1021	GGCTCATCCCGAGGTGGCCCGCCAGTTTCCGAGCCCATGCTGCTGCTGCTGCTGCTG	1080
Db	1021	GGCTCATCCCGAGGTGGCCCGCCAGTTTCCGAGCCCATGCTGCTGCTGCTGCTGCTG	1080
Qy	1081	GGCTGGGTGTCACCTGTGGGCCATGCTCCACAAACAGCCACCTGCTGGGTGCTGCTG	1140
Db	1081	GGCTGGGTGTCACCTGTGGGCCATGCTCCACAAACAGCCACCTGCTGGGTGCTGCTG	1140
Qy	1141	CCCTGTGGAGGTCTGCTGGCAGCTCCACTGGCTTTTCCAGTCCCTCTTCTTCTCCCTGG	1200



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Best Local Similarity 99.9%; Pred. No. 0;
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DB 61 GAGAGTTCACCTGTCTCTCAGGAACACCTGAGCCACAGATCCTGTGGGCAAGCCAGGG 120

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QY 181 GTCCCTCCACGGCCAGGCACCGTGGTCCGACTCAACAGGAGCAGATTCAGTACGTGTCTG 240
DB 181 GTCCCTCCACGGCCAGGCACCGTGGTCCGACTCAACAGGAGCAGATTCAGTACGTGTCTG 240

QY 241 AAATTGGGAAAGCCCTCTCCAGCGGCGCTGAGGTCACTGTCCCTCATTTCTGGAAT 300
DB 241 AAATTGGGAAAGCCCTCTCCAGCGGCGCTGAGGTCACTGTCCCTCATTTCTGGAAT 300

QY 301 GGAGTGGAGAGGCGCTTCAGCCACAGAGATCCGGATTCGGATTCGGATTCGGATTCGGATTC 360
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DB 421 TCAAGGTCTTTGCGGCGCCAGAGAGCCCTGAGAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTG 480

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PR 06-SEP-1998; 98US-0102965P.  
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PR 09-SEP-1998; 98US-00168978.

Query Match 99.2%; Score 1816.8; DB 7; Length 1820;  
Best Local Similarity 99.9%; Pred. No. 0;

Matches 1818; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
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DB	1	GCCTTATAAAGTAGCCTCTCTGATCTGCTCTCTCGGCGAGAGAGGCTACCCCTGGGGCT	60
QY	61	GAGAGTTACCTCTCTCAGAAACCACTGAGCCACAGATCTCTGTGGGAGGCGCCAGGG	120
DB	61	GAGAGTTACCTCTCTCAGAAACCACTGAGCCACAGATCTCTGTGGGAGGCGCCAGGG	120
QY	121	CAGCCATGGCTTTGGGCAAGTAGGCTGGGCTCTGCTGGCACTGCTGCTGCCCGTGGTGG	180
DB	121	CAGCCATGGCTTTGGGCAAGTAGGCTGGGCTCTGCTGGCACTGCTGCTGCCCGTGGTGG	180
QY	181	GTGCTCTCCAGCCAGGCAACCGTGTGGGCTCAACAGAGGAGCAATGAGCTAGCTGTCTG	240
DB	181	GTGCTCTCCAGCCAGGCAACCGTGTGGGCTCAACAGAGGAGCAATGAGCTAGCTGTCTG	240
QY	241	AAATTGGGAAAGCCCTCTCTCAAGGAGGCTCTGAGGTCAGTCTGCTCTCAATTTCTGGACT	300
DB	241	AAATTGGGAAAGCCCTCTCTCAAGGAGGCTCTGAGGTCAGTCTGCTCTCAATTTCTGGACT	300
QY	301	GGAGTCGAGAGGCGCTTACGCCACACAGGATCCGATTCGAAATGTCATGTCGCCGCC	360
DB	301	GGAGTCGAGAGGCGCTTACGCCACACAGGATCCGATTCGAAATGTCATGTCGCCGCC	360
QY	361	TCACCTCGAAATCAATGTCTGGTTTCGAGTGGGCTCTGCTGGCAGAGCTAAATTTACTT	420
DB	361	TCACCTCGAAATCAATGTCTGGTTTCGAGTGGGCTCTGCTGGCAGAGCTAAATTTACTT	420
QY	421	TCAGGCTCTTTCGGGCGCCAGAGCCCTGAGTGAGCTGCTGCTGGAACTCTGCTGCTG	480
DB	421	TCAGGCTCTTTCGGGCGCCAGAGCCCTGAGTGAGCTGCTGCTGGAACTCTGCTGCTG	480
QY	481	ACACCGGCTGACCCAGAGCTCATCAGACCCCTCTGCTGCTGCTGCTGCTGCTGCTT	540
DB	481	ACACCGGCTGACCCAGAGCTCATCAGACCCCTCTGCTGCTGCTGCTGCTGCTGCTT	540
QY	541	TATTTCTGGGCGCCAGGCAACGAGTTTGTATGGGCAAGTAAACAGCACTCCACGCGCTGCTG	600
DB	541	TATTTCTGGGCGCCAGGCAACGAGTTTGTATGGGCAAGTAAACAGCACTCCACGCGCTGCTG	600
QY	601	TGCTGTGAGAGGCAATTAAGCTGTCTGTAGTAAACAGCTGTGCTGAGCACTCTCA	660
DB	601	TGCTGTGAGAGGCAATTAAGCTGTCTGTAGTAAACAGCTGTGCTGAGCACTCTCA	660
QY	661	ACCTGTGAGAGGTCATATGTCACCTGGGCACTTAATGAGCTCAACCCGCTGGCTC	720
DB	661	ACCTGTGAGAGGTCATATGTCACCTGGGCACTTAATGAGCTCAACCCGCTGGCTC	720
QY	721	CTGAGTCCAGATCCGCTATTCATGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCT	780
DB	721	CTGAGTCCAGATCCGCTATTCATGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCT	780
QY	781	CCCTGAGAGTCAATGCTGTCTCTCTGCTGGGCAACCCCACTCACTGCTGCTGCTGCT	840
DB	781	CCCTGAGAGTCAATGCTGTCTCTCTGCTGGGCAACCCCACTCACTGCTGCTGCTGCT	840
QY	841	CCACCCCTTTTGTGTTGCCAAGGCACTGGGTACCGAGGCTCCATGCGCAACGCTGGCC	900
DB	841	CCACCCCTTTTGTGTTGCCAAGGCACTGGGTACCGAGGCTCCATGCGCAACGCTGGCC	900
QY	901	TCTCCAGCAGCTGTTTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	960
DB	901	TCTCCAGCAGCTGTTTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	960
QY	961	TGGACATCAACAGGAGCTGAGGTGGATGCAACACTGCTGCAACACTTGTCTGCTGGGCC	1020
DB	961	TGGACATCAACAGGAGCTGAGGTGGATGCAACACTGCTGCAACACTTGTCTGCTGGGCC	1020
QY	1021	GGCTCATCCGAGGTCGCCGCAATTTCCGAGGCCATGCTGTGTGCTCAAGGTGC	1080
DB	1021	GGCTCATCCGAGGTCGCCGCAATTTCCGAGGCCATGCTGTGTGCTCAAGGTGC	1080

QY	1081	GGCTGGGTGCCACACCTGTGGCCATGCTCCACAAACAAAGCCACCTGGGCTGGCAGC	1140
DB	1081	GGCTGGGTGCCACACCTGTGGCCATGCTCCACAAACAAAGCCACCTGGGCTGGCAGC	1140
QY	1141	CTTTGTGGAGGTCTTGGCCACAGCCTCCAACTCGGCTTTCCAGTCCCTCTTCTCCCTGG	1200
DB	1141	CTTTGTGGAGGTCTTGGCCACAGCCTCCAACTCGGCTTTCCAGTCCCTCTTCTCCCTGG	1200
QY	1201	ATGTGTAGTGAACCTGAGACTCCAGCTCTCTGTGTCCAGGTGAGCTTCAGGGGACCA	1260
DB	1201	ATGTGTAGTGAACCTGAGACTCCAGCTCTCTGTGTCCAGGTGAGCTTCAGGGGACCA	1260
QY	1261	CGTCTGTCTGGGGATGTCCAGCTCAAGTGGGCTCTCTCCAAAGTGGGCTTCATGATA	1320
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QY	1321	CAGATCAGGTGGGCACTGATGGGCAACCGTTTTGGAGAGCCCTCTGTGACCATCTCA	1380
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QY	1441	CTGAGATCTTTGTCTATGAGGCTACGTGTGATATCCAGTGGACTCTTCTACAGAGCT	1500
DB	1441	CTGAGATCTTTGTCTATGAGGCTACGTGTGATATCCAGTGGACTCTTCTACAGAGCT	1500
QY	1501	GAGGCAAGACCACTGGGAGCCCTGAGAGTGGGCGAGCTCGCTCTGCTAGGGGAAATTTCTCA	1560
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DB	1681	CTTTCCCTTCT	1740
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DB	1741	CCACCCCGAGGGGAGCAGACTGCTCCAGCTGTATAGACCTGCGCTCTTGGCAATTA	1800
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DB	1801	AACAACTTCTCTGAGCTGC	1820

## RESULT 13

ACC89598  
ID ACC89598 standard; cDNA; 1820 BP.

XX ACC89598;

XX 11-AUG-2003 (first entry)

XX Human secreted polypeptide PRO5776-encoding cDNA, SEQ ID NO:497.

XX Human; PRO; secreted protein; transmembrane protein;  
XX extracellular domain; tumour necrosis factor-alpha; TNF-alpha;  
XX chondrocyte; proliferation; differentiation; cartilage disorder;  
XX bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;  
XX adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;  
XX liver; drug screening; transgenic animal; genetic analysis;  
XX antiarthritic; vulnary; gene therapy; gene; ss.

OS Homo sapiens.



PR 02-SEP-1998; 98US-0098821P.  
PR 02-SEP-1998; 98US-0098843P.  
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Query Match 99.2%; Score 1816.8; DB 7; Length 1820;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 18:8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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QY 421 TCAAGGCTCTTTCGGGCCCCAGAGCCCTGGAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTG 480  
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QY 481 ACACCGCGTAGCCAGAGCTCCATCAGGACCCCTGTGGTTCAGCATCTCTGCTGCTGCTT 540  
DB 481 ACACCGCGTAGCCAGAGCTCCATCAGGACCCCTGTGGTTCAGCATCTCTGCTGCTGCTT 540  
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DB 781 CCCTGGAAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840  
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DB 841 CCACCCCTTTTGTGTCAGGCACTGGGTACCGAGGCTCCATGGCCACCGTGGGCC 900  
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DB 901 TCTCCAGCAGCTGTTGACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960  
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DB 1141 CTTCTGCTGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200  
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DB 1261 GGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320  
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QY 1381 ATGCTCTTTCGGCCATGGGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440  
DB 1381 ATGCTCTTTCGGCCATGGGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440  
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QY 1501 GAGGCAAGACCTGCTGAGAGGCTGCTGAGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560  
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Db 1801 AACAACTTCTCTGAGCTGC 1820
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RESULT 14
ACA98389
ID ACA98389 standard; cDNA; 1820 BP.
XX
AC ACA98389;
XX
DT 25-JUL-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO5776 cDNA.
XX
KW Human; secreted and transmembrane protein; PRG; transgenic animal;
KW knockout; chromosome identification; tissue typing; tumour;
KW chondrocyte proliferation; chondrocyte differentiation;
KW tumor necrosis factor-alpha release stimulator; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003036144-A1.
XX
PD 20-FEB-2003.
XX
PE 01-JUL-2002; 2002US-00187601.
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PF 18-SEP-1997; 97US-0059263P.
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PF 17-OCT-1997; 97US-0062250P.
PF 21-OCT-1997; 97US-0063486P.
PF 24-OCT-1997; 97US-0063120P.
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DB	121	CAGCCATGGCTTGGGCAAGTAGCTGGCGCTGCTGTGCACTGCTGCTGCCGCTGGTCG 180
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DB	181	GTGCTCCAGCGCAGACCGTGGTCCGACTCAACAAGGCGACATTCAGCTACGTGTCTG 240
QY	241	AAATTGGGAAGCCCTCTCCAGCGGCGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCT 300
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DB	301	GGAGTGGAGAGCGCTTCAGCCCCAGGATCCGAGATTCGGAATTCGGAATTCGATTCCT 360
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DB	361	TCCACCTGAAATTCATTCGTTGGTTCGGAGTGGCGCTGCTGCTGCTGCTGCTGCTGCT 420
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DB	421	TCAGGTCTTTGCGGCCCCAGAGCCCTGAGCTGACGCTGCTGCTGCTGCTGCTGCTGCTG 480
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DB	481	ACACCGGTGACCCAGAGCTTCATCAGGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY	541	TATTTCTGGGCGCAGCCAGAGTTGATGGCAGTAAACAGCACTCCCGCAGCGCTGCTG 600
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DB	601	TCTGCTGAGAGCACAATTAAAGCTGTCTTGAAGTAAACAGCTGTGCTGCTGCTGCTGCT 660
QY	661	ACCTGTGTCAGGGTGTCAATGTCCACTGGGACCTTAATTTGGCTCAACCCGCTGGGTC 720
DB	661	ACCTGTGTCAGGGTGTCAATGTCCACTGGGACCTTAATTTGGCTCAACCCGCTGGGTC 720
QY	721	CTGAGTCCACAGATCCGCTATTTCATGGTCAAGTGTGCCACTGTACAGCTGACTACATTT 780
DB	721	CTGAGTCCACAGATCCGCTATTTCATGGTCAAGTGTGCCACTGTACAGCTGACTACATTT 780
QY	781	CGCTGGAATCAATGCTGTCTCTCTGCTGGGCAAGCCCATCATCTGCTGCCAAGGATG 840
DB	781	CGCTGGAATCAATGCTGTCTCTCTGCTGGGCAAGCCCATCATCTGCTGCCAAGGATG 840
QY	841	CCACCCCTTTTGTGTGTCAGGCAAGCATGTGGGTACCGAGGCTCCATGGCCACCGTGGGC 900
DB	841	CCACCCCTTTTGTGTGTCAGGCAAGCATGTGGGTACCGAGGCTCCATGGCCACCGTGGGC 900
QY	901	TCTCCAGCAGCTGTTTGACTCTGGGCTCCTGCTGCTGCGAGAGGCGCGGTGCGCTCAACC 960
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RESULT 15

AC94031

ID AC94031 standard; cDNA; 1820 BP.

AC AC94031;

XX AC94031;

XX 18-JUL-2003 (first entry)

DE Human secreted/transmembrane protein (2R) cDNA #249.

XX Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;

XX proliferation; differentiation; chondrocyte cell; TNF-alpha;

KW

KW tumour necrosis factor-alpha; gene therapy.  
 XX Homo sapiens.  
 OS US2003036149-A1.  
 XX PD 20-FEB-2003.  
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 PF 02-JUL-2002; 2002US-00187746.  
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 PR 18-SEP-1997; 97US-0059263P.  
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Search completed: June 29, 2004, 21:57:47  
Job time : 1066 secs



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; Sequence 9156, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9156
; LENGTH: 1839
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9156

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Query Match	2.5%; Score 46.6; DB 4; Length 1839;
Best Local Similarity	48.6%; Pred. No. 0.024;
Matches	158; Conservative 0; Mismatches 164; Indels 3; Gaps 1;
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QY	953 CCTCAACCTTGGACATCACAGGCGAGCTGAGGTCCGATGACAACTCTCTGAACACCTCTGC 1012
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1491	CGCGGCCCTCGACGCGCGACACCGCGCTGAAGATGCAGACCTTCTCTCTGGACGTATGGGC 1550
QY	1013 TCTGGGCGGGCTCA---TCCGAGAGTGGCCGCGCCAGATTCCGAGCCCATGCTCTGGT 1069
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RESULT 4

US-09-252-991A-9071

Sequence 9071, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

Best Local Similarity 61.9%; Pred. No. 0.019;  
Matches 73; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

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1690	CCCTCCCTCTTCTCCTCCCTCTCCCTCATCTCCCTCCCTCTCTCTGCCGACCC	1747
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US-09-252-991A-8423/c
/ Sequence 8423, Application US/09252991A
/ Patent No. 6551795
/ GENERAL INFORMATION:
/ APPLICANT: Marc J. Rubenfield et al.
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
/ TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: 107196.136
/ CURRENT APPLICATION NUMBER: US/09/252,991A
/ CURRENT FILING DATE: 1999-02-18
/ PRIOR APPLICATION NUMBER: US 60/374,788
/ PRIOR FILING DATE: 1998-02-18
/ PRIOR APPLICATION NUMBER: US 60/394,190
/ PRIOR FILING DATE: 1998-07-27
/ NUMBER OF SEQ ID NOS: 33142
/ SEQ ID NO 8423
/ LENGTH: 1761
/ TYPE: DNA
/ ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8423

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RESULT 9

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US-09-252-991A-14215
; Sequence 14215, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 14215
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-14215

Query Match      2.5%; Score 45.2; DB 4; Length 1257;
Best Local Similarity 43.9%; Pred. No. 0.047;
Matches 194; Conservative 0; Mismatches 248; Indels 0; Gaps 0;

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420	DB	CACCACAGGCGCTGCTGCGGAACTTGGTACCGGCGCGGCTGTTCGCGCGCGGTGCGCGC	479
848	QY	TTTTGTGTTGCCAAGGCATGTGGGTACCGAGGCTCCATGGGCACCGTGGGCGCTTCCCA	907
480	DB	TTGGCTTCGGCGATGCAGCGCGCACCATGCGCGCCGCGCGCTCGCGGCGCTGCTCTA	539
908	QY	GCAGCTGTTTGACTCTGCGCTCTGCTGCTGCAGAGGCGGTTGCCTCAACTGGACAT	967
540	DB	TGCGTTGCGTGCCCTCTCTGGTCTACGTGCCGACCGCGACTCTCTACGTCTCGCTGCGT	599
968	QY	CACAGGCGAGCTGAGTTCGGATGACAACTGCTGAACACTCTGCTGGCGCGGCTCAT	1027
600	DB	CCTGACGCTCAGCCTSCCGGTACGCAACACAGCGGCTCACCCAGGGCAAGGCCACCCCTGA	659
1028	QY	CCGGAGGTGGCCCGCAGTTTCCGAGCGCATGCTCTGTGTGCTCAAGGTGCGGCTGGG	1087
660	DB	CTCGCTCTCGCGGATCCGTTTTCATCCGCGACCGACCCGACATCTTGGGGCAATCTC	719
1088	QY	TGCCACACTGTGGCCATGCTCCACACAAACACCGCACCTCTCGCGCTGCAGGCGCTTCGT	1147
720	DB	CCTTGACCTGTTGCGCGTGTCTCTCGCGGGGCGCACCGCCCTGCTCCGGTGTGCGCAA	779
1148	QY	GGAGGTCTGGGCACAGCCTCC	1169
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## RESULT 10

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US-09-252-991A-14171
; Sequence 14171: Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Yarc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107195.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 14171
; LENGTH: 1266
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-14171

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	Query Match	2.5%;	Score 45.2;	DB 4;	Length 1266;
	Best Local Similarity	43.9%;	Pred. No. 0.047;		
	Matches 194;	Conservative 0;	Mismatches 248;	Indels 0;	Gaps 0;
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DB	397	CAACATGATCTTC	CTCGCTCTCGCCCTCGGTATCCGCCCGCCGCTTCGAAATGCGAC		456
QY	788	AGTCAATGCTGTCTT	CTCTCTCTGTGGGCAAGCCCATCATCTCTGCCCCACGATGCCACCCC		847
DB	457	CACCCAGGCGCTGCT	GTCCGAACTGTGTACCGGCGGGCTGTTCGCGCGCGGTGGCCCGC		516
QY	848	TTTGTGTTGCCAAGSCAT	GTGGGTACCGAGGCGTCCATGGCGCACCGTGGGCGCTCTCCCA		907
DB	517	TTCCGGCTCGCGCAT	GCAGCGCGGACCATTCGCCGCCCGGCCCTCGCGGCGTGTCTTA		576
QY	908	GCAGCGTGTGATCT	GTGCGCTCTGTGTGCAGAAAGCGCGTGCGCCCTCAA	CTTGACAT	967
DB	577	TGCGTTCGGTGTGCT	CTCTGGGTCTAGCTGCGGACCGCGACTCTCTAGTCTCTCGCGTGGCT		636

QY 968 CACAGGCGAGCTGAGTGGATGACAACTGCTGACACCTCTGCTCTCTGCGCGGCTCAT 1027  
DB 637 CTTGACGCTCAGCTGCGGTAGGACAGCGCTCTACCCAGGGCAAGCCACCTCGA 696  
QY 1028 CCCGAGGTGGCCCGCAGATTTCCGAGAGCCCAAGCTGTGGTCTCAAGTGGCGGTGGG 1087  
DB 697 CTCGCTGCTCGCGGATCCGTTTCATCCGAGCGGACGAGCATCTTCGGGCAATCTC 756  
QY 1088 TGCCACACTGTGGCCATGCTCCACACAAACGACGCTGCGGCTGACGCTTCTGT 1147  
DB 757 CTTGACCTGTTGCGGCTGCTCTCGGCGGCGCACCGCCCTGCTCCCGGTGTTCGCCAA 816  
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DB 817 GGACATCTGCTCACCGGCGCC 838

RESULT 11  
US-09-252-991A-14052/c  
; Sequence 14052, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 14052  
; LENGTH: 1566  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-14052

Query Match 2.5%; Score 45.2; DB 4; Length 1566;  
Best Local Similarity 43.9%; Pred. No. 3.052;  
Matches 194; Conservative 0; Mismatches 248; Indels 0; Gaps 0;  
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QY 788 AGTCATGCTGTTCTTCTGCTGGGCAAGCCCAATATCTGCCCCACGATGCCACCCC 847  
DB 997 CACCCAGGCGCTGTCGCCGAACCTGGTACCGCGCGGCTGTCCCGCGCGGTGGCGCG 938  
QY 848 TTTGTGTGTCAGGCGATGTGGTACGAGGCTCCATGCCACGCTGGGCTCTCCCA 907  
DB 937 TTGGCTTGGCGATGACAGGCGGACCATTTGCCCGCGCGGCTTCCGCGGCTCTCTA 878  
QY 908 GCAGCTGTTGACTCTGGGCTCTGCTGCTGAGAGGCGGCTGCGCTCAACCTGGACAT 967  
DB 877 TGGCTGCGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 818  
QY 968 CACAGGCGAGCTGAGTGGATGACAACTGCTGAAACCTGCTGCTGCTGCTGCTGCTGCTGCT 1027  
DB 817 CTTGACGCTGAGCTGCGGCTGACGAAACGAGCGGCTACCCAGGCGCAAGGCCACCTCGA 758  
QY 1028 CCGAGGTGGCGCCGAGTTTCCGAGCCCATGCTGTGGTCTCAAGGTGGCGCTGGG 1087  
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QY 1088 TGCCACACTGTGGCCATGCTCCACACAAACGACGCTGCGGCTGCGGCTGCTGCTGCTGCTGCT 1147  
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QY 1148 GGAGTCTCTGGCCACAGCTCC 1169

DB 637 GGACATCTCTCTCACCGGCGCC 616

RESULT 12  
US-08-658-136-2  
; Sequence 2, Application US/08658136  
; Patent No. 6071717  
; GENERAL INFORMATION:

; APPLICANT: KLINGER, KATHERINE W  
; APPLICANT: LANDES, GREGORY M  
; APPLICANT: BURN, TIMOTHY C  
; APPLICANT: CONNORS, TIMOTHY D  
; APPLICANT: DACKOWSKI, WILLIAM  
; APPLICANT: GERMINO, GREGORY  
; APPLICANT: QIAN, FENG  
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: GENZYME CORPORATION  
; STREET: ONE MOUNTAIN ROAD  
; CITY: FRAMINGHAM  
; STATE: MASSACHUSETTS  
; COUNTRY: USA  
; ZIP: 01701  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/658,136  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LASSEN, ELIZABETH  
; REGISTRATION NUMBER: 31,845  
; REFERENCE/DOCKET NUMBER: GEN4-17.8  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 508-872-8400  
; TELEFAX: 508-872-5415  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 53526 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-658-136-2

Query Match 2.5%; Score 45.2; DB 3; Length 53526;  
Best Local Similarity 68.9%; Pred. No. 0.24; Mismatches 0; Gaps 0;  
Matches 62; Conservative 0; Indels 28; Indels 0; Gaps 0;  
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DB 36628 CCCCCTTCT 36687  
QY 1721 CTCCTCCCTCCT 1750  
DB 36688 CTCCT 36717

RESULT 13  
US-08-658-136-1  
; Sequence 1, Application US/08658136  
; Patent No. 6071717  
; GENERAL INFORMATION:  
; APPLICANT: KLINGER, KATHERINE W  
; APPLICANT: LANDES, GREGORY M  
; APPLICANT: BURN, TIMOTHY C  
; APPLICANT: CONNORS, TIMOTHY D  
; APPLICANT: DACKOWSKI, WILLIAM  
; APPLICANT: GERMINO, GREGORY



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Qy     1777 GTATAGACCTGCCCTTTCAT 1798  
  
Db      :: : : : : : : : : : : : : : : : : : :  
        86 SYNYSNYSNYSNYSNYSNYSNYSNYSNYSNY 65
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Job time : 162 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 29, 2004, 21:40:00 ; Search time 1152 Seconds  
(without alignments)  
7307.153 Million cell updates/sec

Title: US-10-069-034-65

Perfect score: 1831

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3031105 seqs, 2298700234 residues

Total number of hits satisfying chosen parameters: 6362210

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 19: /cgn2\_6/prodata/1/pubpna/US60\_PUBCOMB.seq\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1  
US-09-965-529-65  
; Sequence 65, Application US/09965529  
; Publication No. US20020182671A1  
; GENERAL INFORMATION:  
; APPLICANT: LAL, Preeti  
; APPLICANT: YUE, Henry  
; APPLICANT: TANG, Y. Tom  
; APPLICANT: BANDMAN, Olga  
; APPLICANT: BURFORD, Neil  
; APPLICANT: AZIMZAI, Yalda  
; APPLICANT: BAUGHN, Mariah R.  
; APPLICANT: LU, Dyoung Aina M.  
; APPLICANT: PATTERSON, Chandra  
; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS  
; FILE REFERENCE: PF-0731 USA  
; CURRENT APPLICATION NUMBER: US/09/965,529  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 60/149,641; 60/164,203; PCT/US00/22315  
; PRIOR FILING DATE: 1999-08-17; 1999-11-09; 2000-08-14  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PERL Program  
; SEQ ID NO 65  
; LENGTH: 1831  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20020182671A1 3393430CB1  
US-09-965-529-65

Query Match 100.0%; Score 1831; DB 9; Length 1831;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1831; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1561 TTTCAAGCCACTGGGAAACTGAGGCAAAACATATAGTATGATCAGCAAGCTGGAC 1620  
Db 1561 TTTCAAGCCACTGGGAAACTGAGGCAAAACATATAGTATGATCAGCAAGCTGGAC 1620  
Qy 1621 TGCCTAGCTGGGCTGCTTTATCTTCCCTGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680  
Db 1621 TGCCTAGCTGGGCTGCTTTATCTTCCCTGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680  
Qy 1681 CTTTCCCTTCTG 1740  
Db 1681 CTTTCCCTTCTG 1740  
Qy 1741 CCGACCCAGAGGGGAGGAGAGCTGCTCTCCAGGCTGATAGAGCTGCTGCTGCTGCTGCTG 1800  
Db 1741 CCGACCCAGAGGGGAGGAGAGCTGCTCTCCAGGCTGATAGAGCTGCTGCTGCTGCTGCTG 1800  
Qy 1801 AACCACTTCTCTTGAAGCTGCAAAAAA 1831  
Db 1801 AACCACTTCTCTTGAAGCTGCAAAAAA 1831

## RESULT 2

US-09-969-680A-65

; Sequence 65, Application US/09969680A

; Publication No. US20030124649A1

; GENERAL INFORMATION:

; APPLICANT: IAL, Preeti; YUE, Henry

; APPLICANT: TANG, Y. Tom; BANDMAN, Olga

; APPLICANT: BURFORD, Neil; AZIMZAI, Yalda

; APPLICANT: BAUGHN, Mariah R.; LU, Dying Aina M.

; APPLICANT: PATTERSON, Chandra

; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS

; FILE REFERENCE: PP-0731-1 USA

; CURRENT APPLICATION NUMBER: US/09/969,680A

; CURRENT FILING DATE: 2001-10-02

; PRIOR APPLICATION NUMBER: US00/22315

; PRIOR FILING DATE: 2000-08-14

; PRIOR APPLICATION NUMBER: 60/149,641

; PRIOR FILING DATE: 1999-08-17

; PRIOR APPLICATION NUMBER: 60/164,203

; PRIOR FILING DATE: 1999-11-09

; NUMBER OF SEQ ID NOS: 74

; SOFTWARE: PERL Program

; SEQ ID NO 65

```

; LENGTH: 1831
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030:24649A1 3393430CB1
US-09-969-680A-65

Query Match      100.0%; Score 1831; DB 10; Length 1831;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1831; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCTTATAAGTAGCCTCTGCATCTGCCTCGCTCGGAGAGGAGGCTACCTCTGGGSC 60
Db 1 GCCTTATAAGTAGCCTCTGCATCTGCCTCGCTCGGAGAGGAGGCTACCTCTGGGSC 60

Qy 61 GAGAGTTCACCTGTCTCAGGAACACCTGAGCCACAGATCCTGTGGCAGCGGCCAGGG 120
Db 61 GAGAGTTCACCTGTCTCAGGAACACCTGAGCCACAGATCCTGTGGCAGCGGCCAGGG 120

Qy 121 CAGCCATGGCTTGGGCAAGTAGGCTGGGCTGTGCTGGCACTGCTCTGCGCGTGTGCG 180
Db 121 CAGCCATGGCTTGGGCAAGTAGGCTGGGCTGTGCTGGCACTGCTCTGCGCGTGTGCG 180

Qy 181 GTGCCTCCACGCCAGGACCGTGTCCGACTCAA CAAGGCAGCATTTGAGTACGTGTCTG 240
Db 181 GTGCCTCCACGCCAGGACCGTGTCCGACTCAA CAAGGCAGCATTTGAGTACGTGTCTG 240

Qy 241 AATTTGGGAAGCCCTCTCCAGGGGGCTTGCAGGTCACTGTCCCTCATTTCTCTGGACT 300
Db 241 AATTTGGGAAGCCCTCTCCAGGGGGCTTGCAGGTCACTGTCCCTCATTTCTCTGGACT 300

Qy 301 GGAGTGGAGAGGCGCTTCAGCCCAACCAAGGATCCGATTTCTGAATGTCCATGTGCCCGCC 360
Db 301 GGAGTGGAGAGGCGCTTCAGCCCAACCAAGGATCCGATTTCTGAATGTCCATGTGCCCGCC 360

Qy 361 TCACCTGAAATTCATTGTGGTTTCGGAGTGGCCCTGTGGCAGCAGCTAAATTTACTT 420
Db 361 TCACCTGAAATTCATTGTGGTTTCGGAGTGGCCCTGTGGCAGCAGCTAAATTTACTT 420

Qy 421 TCAAGTCTTTTGGCGCCGACAGCCCTTGAGCTGAGCTGCTGTGGGAACCTGTGGCTG 480
Db 421 TCAAGTCTTTTGGCGCCGACAGCCCTTGAGCTGAGCTGCTGTGGGAACCTGTGGCTG 480

Qy 481 ACACCCGCTGACCCAGAGCTCCATCAGGACCCCTGTGTGTCAGCATCTCTGCCTGCTCT 540
Db 481 ACACCCGCTGACCCAGAGCTCCATCAGGACCCCTGTGTGTCAGCATCTCTGCCTGCTCT 540

Qy 541 TATTCTGGGCCACGCCAAGAGTTGATGGCAGTAA CAGCACCTCCACGCTCTCTGG 600
Db 541 TATTCTGGGCCACGCCAAGAGTTGATGGCAGTAA CAGCACCTCCACGCTCTCTGG 600

Qy 601 TCTGTGTGCAAGACACATTAAAGCTGTCTTGAGTAA CAGCTGTGCTGAGCATCTCCA 660
Db 601 TCTGTGTGCAAGACACATTAAAGCTGTCTTGAGTAA CAGCTGTGCTGAGCATCTCCA 660

Qy 661 ACCTGTGTGAGGCTGTCAATGTCCACTGGGCACTTTAATTTGSCCTCAACCCCGTGGCTC 720
Db 661 ACCTGTGTGAGGCTGTCAATGTCCACTGGGCACTTTAATTTGSCCTCAACCCCGTGGCTC 720

Qy 721 CTGAGTCCCAGATCCGCTATTTCATGTCAGTGTGCCACTGTGTCAGTGTGCTGAGTACATTT 780
Db 721 CTGAGTCCCAGATCCGCTATTTCATGTCAGTGTGCCACTGTGTCAGTGTGCTGAGTACATTT 780

Qy 781 CCCTGGAAATCAATGCTGTCTCTTCTGCTGGGAAGGCCATCTATCTGTGCCACGGATG 840
Db 781 CCCTGGAAATCAATGCTGTCTCTTCTGCTGGGAAGGCCATCTATCTGTGCCACGGATG 840

Qy 841 CCACCCCTTTGTGTTGSCCAAGCATGTGGTACCGAGGCTCCATGTGCCACCGTGGCC 900
Db 841 CCACCCCTTTGTGTTGSCCAAGCATGTGGTACCGAGGCTCCATGTGCCACCGTGGCC 900

Qy 901 TCTCCAGCAGCTGTTTGACTCTGCGCTCTGCTGTGTCAGAGGCGGCTGCTCAAC 960

```



Db 1501 GAGGCAAGACCACTGGAGGCGCTGAGAGTGGGCGAGCTCGCTGCTCAGGCGAATTTCTCA 1560  
Qy 1561 TTTCAGGCACTGGGMAACTGAGCAAAACATAGTCTAGTATCATCAACAAAGCTGGAC 1620  
Db 1561 TTTCAGGCACTGGGMAACTGAGCAAAACATAGTCTAGTATCATCAACAAAGCTGGAC 1620  
Qy 1621 TCTTAGCTGGGCTGTTTTATCTTCCCTGAGTGGCTGCTCCCTCCCTCACTTCTGCC 1680  
Db 1621 TGCTTAGCTGGGCTGTTTTATCTTCCCTGAGTGGCTGCTCCCTCCCTCACTTCTGCC 1680  
Qy 1681 CTTTCCCTTCCCTCCCTCTTCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 1740  
Db 1681 CTTTCCCTTCCCTCCCTCTTCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 1740  
Qy 1741 CCACCCAGGGGGGAGAGAGTCTCTCCCTGAGTGGCTGCTCCCTCCCTCCCTCCCTCCCT 1800  
Db 1741 CCACCCAGGGGGGAGAGAGTCTCTCCCTGAGTGGCTGCTCCCTCCCTCCCTCCCTCCCT 1800  
Qy 1801 AACAACTTCTCTTGAGCTGC 1820  
Db 1801 AACAACTTCTCTTGAGCTGC 1820

## RESULT 4

US-10-199-670-497  
; Sequence 497, Application US/10199670  
; Publication No. US20040033560A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3430R1C401  
; CURRENT APPLICATION NUMBER: US/10/199,670  
; PRIOR FILING DATE: 2002-07-19  
; PRIOR APPLICATION NUMBER: 10/052586  
; PRIOR FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059266  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063120  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063121  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063486  
; PRIOR FILING DATE: 1997-10-21  
; PRIOR APPLICATION NUMBER: 60/063540  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063541  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063544  
; PRIOR FILING DATE: 1997-10-28  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 497  
; LENGTH: 1820  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-199-670-497

Query Match

99.2%; Score 1816.8; DB 13; Length 1820;

Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1818; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 GCCTTATAAGTAGCCTCTGCACTGCTGCTCGGCGAGAGAGGCTACCTCGGGCT 60  
Db 1 GCCTTATAAGTAGCCTCTGCACTGCTGCTCGGCGAGAGAGGCTACCTCGGGCT 60  
Qy 61 GAGAGTTCACCTGCTCTCAGAACCACTGAGGCCACAGATCCCTGAGGAGGCGGCGG 120  
Db 61 GAGAGTTCACCTGCTCTCAGAACCACTGAGGCCACAGATCCCTGAGGAGGCGGCGG 120  
Qy 121 CAGCCATGCTTGGGCAAGTAGGCTGGGCTGCTGCTGCGCACTGCTGCTGCGGCTG 180  
Db 121 CAGCCATGCTTGGGCAAGTAGGCTGGGCTGCTGCTGCGCACTGCTGCTGCGGCTG 180  
Qy 181 GTGCTTCCACGCGAGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
Db 181 GTGCTTCCACGCGAGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
Qy 241 AAATTGGGAAAGCCCTCTCAGCGGGGCTGAGTCACTGCTGCTGCTGCTGCTGCT 300  
Db 241 AAATTGGGAAAGCCCTCTCAGCGGGGCTGAGTCACTGCTGCTGCTGCTGCTGCT 300  
Qy 301 GGAGTGGAGAGGCGCTTCAGCCCAAGGATCCGATTCGATGCTCAGATGCTGCTGCT 360  
Db 301 GGAGTGGAGAGGCGCTTCAGCCCAAGGATCCGATTCGATGCTCAGATGCTGCTGCT 360  
Qy 361 TCCACCTGAAATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
Db 361 TCCACCTGAAATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
Qy 421 TCAAGTCTTTCGCGCCCGAGAGCCCTGAGGCTGAGCTGCTGCTGCTGCTGCTGCTG 480  
Db 421 TCAAGTCTTTCGCGCCCGAGAGCCCTGAGGCTGAGCTGCTGCTGCTGCTGCTGCTG 480  
Qy 481 ACACCCGCTGACCCAGAGCTCCATCAGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
Db 481 ACACCCGCTGACCCAGAGCTCCATCAGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
Qy 541 TATTCCTGGGCGACCGCCAAAGGTTGATGAGTAAAGCACTGCTGCTGCTGCTGCTGCT 600  
Db 541 TATTCCTGGGCGACCGCCAAAGGTTGATGAGTAAAGCACTGCTGCTGCTGCTGCTGCT 600  
Qy 601 TCCTGCTCAGAGCACATTAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660  
Db 601 TCCTGCTCAGAGCACATTAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660  
Qy 661 ACCTGCTCAGAGGCTCAATGTCCAACCTGGGCACTTAAATGGGCTCAACCCCGTGG 720  
Db 661 ACCTGCTCAGAGGCTCAATGTCCAACCTGGGCACTTAAATGGGCTCAACCCCGTGG 720  
Qy 721 CTGAGTCCAGATCCGCTTATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
Db 721 CTGAGTCCAGATCCGCTTATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
Qy 781 CCCTGGAAGTCAATGCTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840  
Db 781 CCCTGGAAGTCAATGCTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840  
Qy 841 CCACCCCTTTTGTGTTGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
Db 841 CCACCCCTTTTGTGTTGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
Qy 901 TCTCCAGAGCTGTTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
Db 901 TCTCCAGAGCTGTTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
Qy 961 TGGACATCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020  
Db 961 TGGACATCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020  
Qy 1021 GCTCATCCGAGGCTGGCGCCAGCTTTCGAGGCCATGCTGCTGCTGCTGCTGCTGCTGCT 1080  
Db 1021 GCTCATCCGAGGCTGGCGCCAGCTTTCGAGGCCATGCTGCTGCTGCTGCTGCTGCTGCT 1080

Db 1021 GGCTCAATCCCGAGGTGGCCCCAGATTCCGAGCCCCATGCTGTGGTCTCAAAGTGC 1080  
Qy 1081 GGCTGGTGGCCACACCTGTGGCCATGCTCCACACAAACAAAGCCACCTGGGCTCAGC 1140  
Db 1082 GGCTGGTGGCCACACCTGTGGCCATGCTCCACACAAACAAAGCCACCTGGGCTCAGC 1140  
Qy 1141 CTTTGTGGAGTCTCTGGCCACAGCTCCAACTGGGCTTCAGTCCCTCTTCTCCCTGG 1200  
Db 1142 CTTTGTGGAGTCTCTGGCCACAGCTCCAACTGGGCTTCAGTCCCTCTTCTCCCTGG 1200  
Qy 1201 ATGTGTAGTGAATTTGAGCTCCAGCTCTGTGTCACAAAGTGGAGCTTCAGGGACCA 1260  
Db 1202 ATGTGTAGTGAATTTGAGCTCCAGCTCTGTGTCACAAAGTGGAGCTTCAGGGACCA 1260  
Qy 1261 CTTTGTGGTGGGATGTCAGCTCAGCTCAGCTGAGCTCCCTCCAAAGTGGGCTTCATTGATA 1320  
Db 1262 CTTTGTGGTGGGATGTCAGCTCAGCTCAGCTGAGCTCCCTCCAAAGTGGGCTTCATTGATA 1320  
Qy 1321 CAGATCAGTGGGACACATGATGGGACCGTTTTTGAAGCCCTGTGGACCAATCTCA 1380  
Db 1322 CAGATCAGTGGGACACATGATGGGACCGTTTTTGAAGCCCTGTGGACCAATCTCA 1380  
Qy 1381 ATGCTCTTGGCCATGGGAATTGCCCTCCCTGGTGTGTCAACTCCACTATGTGCC 1440  
Db 1382 ATGCTCTTGGCCATGGGAATTGCCCTCCCTGGTGTGTCAACTCCACTATGTGCC 1440  
Qy 1441 CTGAGATCTTTGTCTATGAGGCTACGTGGTGTATATCCAGTGGACTCTTACCAAGACT 1500  
Db 1442 CTGAGATCTTTGTCTATGAGGCTACGTGGTGTATATCCAGTGGACTCTTACCAAGACT 1500  
Qy 1501 GAGGCAACACCTGGGAGCTGTGAGTGGGCGAGCTGTGCTCAGCGAATTTCTCA 1560  
Db 1502 GAGGCAACACCTGGGAGCTGTGAGTGGGCGAGCTGTGCTCAGCGAATTTCTCA 1560  
Qy 1561 TTTCAGGCACTGGGAACTGAGGCAAAACATATAGTATCATCAACCAAGCTGGAC 1620  
Db 1562 TTTCAGGCACTGGGAACTGAGGCAAAACATATAGTATCATCAACCAAGCTGGAC 1620  
Qy 1621 TGCTAGTGGGCTGTTTATCTTCCCTGAGTGGCTGGGCTCTCCCTCACTTCTGCC 1680  
Db 1622 TGCTAGTGGGCTGTTTATCTTCCCTGAGTGGCTGGGCTCTCCCTCACTTCTGCC 1680  
Qy 1681 CTTTCCCTTCCCT 1740  
Db 1682 CTTTCCCTTCCCT 1740  
Qy 1741 CCCACCCAGGGGAGGAGAGTGTCTCTCAGGCTGTATAGAGCTGCCCTCTTGCATTA 1800  
Db 1742 CCCACCCAGGGGAGGAGAGTGTCTCTCAGGCTGTATAGAGCTGCCCTCTTGCATTA 1800  
Qy 1801 AACAACTTCTCTGAGTGC 1820  
Db 1802 AACAACTTCTCTGAGTGC 1820

## RESULT 5

US-10-201-858-497

; Sequence 497, Application US/10231858

; Publication No. US20040038337A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P3430R1C464  
CURRENT APPLICATION NUMBER: US/10/201,858  
CURRENT FILING DATE: 2002-07-23  
PRIOR APPLICATION NUMBER: 10/052586  
PRIOR FILING DATE: 2002-01-15  
PRIOR APPLICATION NUMBER: 60/059263  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/059266  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063120  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063121  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063486  
PRIOR FILING DATE: 1997-10-21  
PRIOR APPLICATION NUMBER: 60/063540  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063541  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063544  
PRIOR FILING DATE: 1997-10-28  
Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 612  
SEQ ID NO 497  
LENGTH: 1820  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-201-858-497

Query Match 99.2%; Score 1816.8; DB 13; Length 1820;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1818; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCCTTATAAGTAGCTCTGATATGCTGCTCGGGCAGAGAGGGTACCTGGGGCT 60  
Db 1 GCCTTATAAGTAGCTCTGATATGCTGCTCGGGCAGAGAGGGTACCTGGGGCT 60  
Qy 61 GAGAGTTCACCTGTCTCAGGACCACTGAGCCCAAGATCTGTGGGAGCGGCGG 120  
Db 61 GAGAGTTCACCTGTCTCAGGACCACTGAGCCCAAGATCTGTGGGAGCGGCGG 120  
Qy 121 CAGCATGCTTGGCAAGTAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180  
Db 121 CAGCATGCTTGGCAAGTAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180  
Qy 181 GTGCTTCCACCGCAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
Db 181 GTGCTTCCACCGCAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
Qy 241 AAATTGGGAAAGCCCTCTCCAGGGGGCCCTGAGGTCACCTGCTGCTGCTGCTGCTG 300  
Db 241 AAATTGGGAAAGCCCTCTCCAGGGGGCCCTGAGGTCACCTGCTGCTGCTGCTGCTG 300  
Qy 361 TCCACCTGAAATTCATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420  
Db 361 TCCACCTGAAATTCATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420  
Qy 421 TCAAGTCTTTCGGGGCCCGCAGAGCCCTGAGGCTGAGCTGAGCTGAGCTGAGCTGAG 480  
Db 421 TCAAGTCTTTCGGGGCCCGCAGAGCCCTGAGGCTGAGCTGAGCTGAGCTGAGCTGAG 480  
Qy 481 ACACCCGCTGACCCAGAGCTTCCATCAGGACCCCTGCTGCTGCTGCTGCTGCTGCTG 540  
Db 481 ACACCCGCTGACCCAGAGCTTCCATCAGGACCCCTGCTGCTGCTGCTGCTGCTGCTG 540  
Qy 541 TATCTCTGGGCGCAGCCCAAGAGTTGATGGCAGTAACAGACCTCCGACGGGCTGCTG 600









1381 ATGCTCTCTTGCCCATGGAAATGGCTCCCTGGTGTGGTCAACCTCCACTATGTGGCC 1440  
Db ATGCTCTCTTGCCCATGGAAATGGCTCCCTGGTGTGGTCAACCTCCACTATGTGGCC 1440  
1441 CTGAGATCTTTGTCTATGAGGGCTACGTGGTGATATCCAGTGGACTCTTCTACAGAGCT 1500  
Db CTGAGATCTTTGTCTATGAGGGCTACGTGGTGATATCCAGTGGACTCTTCTACAGAGCT 1500  
1501 GAGCAAGACCACTGGGAGGCTGAGAGTGGGCCAGCTCGCTGTCTCAGGCGAATTTCTCA 1560  
Db GAGCAAGACCACTGGGAGGCTGAGAGTGGGCCAGCTCGCTGTCTCAGGCGAATTTCTCA 1560  
1561 TTCAAGCACTGGGAACTGAGGCAAAACCATATCTAGTCAATCAACCAAGCTGGAC 1620  
Db TTCAAGCACTGGGAACTGAGGCAAAACCATATCTAGTCAATCAACCAAGCTGGAC 1620  
1621 TGCTAGTGGGCTTTTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1680  
Db TGCTAGTGGGCTTTTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1680  
1681 CT 1740  
Db CT 1740  
1741 CCCACCCAGGGGGAGCAGACTCTCTCTCAGGCTGTATAGACTTGCCTCTTTCATTA 1800  
Db CCCACCCAGGGGGAGCAGACTCTCTCTCAGGCTGTATAGACTTGCCTCTTTCATTA 1800  
1801 AACAACTCTCTGAGCTGC 1820  
Db AACAACTCTCTGAGCTGC 1820

## RESULT 7

US-10-205-890-497  
Sequence 497, Application US/10205890  
Publication No. US20040048334A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Chen, Jian  
APPLICANT: Desnoyers, Luc  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Pan, James  
APPLICANT: Smith, Victoria  
APPLICANT: Matanabe, Colin K.  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3430R1C519  
CURRENT APPLICATION NUMBER: US/10/205,890  
CURRENT FILING DATE: 2002-07-26  
PRIOR APPLICATION NUMBER: 10/052586  
PRIOR FILING DATE: 2002-01-15  
PRIOR APPLICATION NUMBER: 60/059263  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/059266  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063120  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063121  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063486  
PRIOR FILING DATE: 1997-10-21  
PRIOR APPLICATION NUMBER: 60/063540  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063541  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063544

PRIOR FILING DATE: 1997-10-28  
Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 612  
SEQ ID NO 497  
LENGTH: 1820  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-205-890-497

Query Match 99.2%; Score 1816.8; DB 13; Length 1820;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1818; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 GCCTTATAAGTAGCTCTGCTCATCTGCTGCTGGGAGGAGGAGGCTTACCTGGGGCT 60  
Db 1 GCCTTATAAGTAGCTCTGCTCATCTGCTGCTGGGAGGAGGAGGCTTACCTGGGGCT 60  
61 GAGAGTTTCACTGTCTCAGGAACCACTGAGCCACAGATCCTGTGGGAGCGGCCAGGG 120  
Db 61 GAGAGTTTCACTGTCTCAGGAACCACTGAGCCACAGATCCTGTGGGAGCGGCCAGGG 120  
121 CAGCATGGCTTGGGAGTAGGCTGGGCTGTGCTGTGGACTGTGCTGCTGCTGCTGCTG 180  
Db 121 CAGCATGGCTTGGGAGTAGGCTGGGCTGTGCTGTGGACTGTGCTGCTGCTGCTGCTG 180  
181 GTGCTTCCAGCCAGGACAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
Db 181 GTGCTTCCAGCCAGGACAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
241 AAATTGGGAAAGCCCTTCCAGCGGGCCCTGAGAGTCACTGTGCTGCTGCTGCTGCTG 300  
Db 241 AAATTGGGAAAGCCCTTCCAGCGGGCCCTGAGAGTCACTGTGCTGCTGCTGCTGCTG 300  
301 GGAGTGGAGAGCGGCTTCCAGCCAGGAGTCCGAGTCTGAAATGCTGATGCTGCTGCTG 360  
Db 301 GGAGTGGAGAGCGGCTTCCAGCCAGGAGTCCGAGTCTGAAATGCTGATGCTGCTGCTG 360  
361 TCCACCTGMAATTCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
Db 361 TCCACCTGMAATTCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
421 TCAAGTCTTTTGGGCCCCAGAGCCCTTGGAGTCACTGCTGCTGCTGCTGCTGCTGCTG 480  
Db 421 TCAAGTCTTTTGGGCCCCAGAGCCCTTGGAGTCACTGCTGCTGCTGCTGCTGCTGCTG 480  
481 ACACCCGGTGACCCAGAGTCCATCAGGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 540  
Db 481 ACACCCGGTGACCCAGAGTCCATCAGGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 540  
541 TATTCTGGGCCCCAGCCAGAGTTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
Db 541 TATTCTGGGCCCCAGCCAGAGTTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
601 TCTGTTGAGAGAGCATTAAAGCTCTCTTGGTAAAGCTGCTGCTGCTGCTGCTGCTGCTG 660  
Db 601 TCTGTTGAGAGAGCATTAAAGCTCTCTTGGTAAAGCTGCTGCTGCTGCTGCTGCTGCTG 660  
661 ACCTGTTGAGAGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720  
Db 661 ACCTGTTGAGAGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720  
721 CTGAGTCCAGAGTCCGCTATTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
Db 721 CTGAGTCCAGAGTCCGCTATTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
781 CCTTGAAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840  
Db 781 CCTTGAAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840  
841 CCACCCCTTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
Db 841 CCACCCCTTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900



Qy	421	TC	AAGGTC	TTTTGGCGCC	CCAGAGCC	CTGGAGCT	GACG	CTGCTG	CTGTGAA	CTGCTGGCTG	480
Db	421	TC	AAGGTC	TTTTGGCGCC	CCAGAGCC	CTGGAGCT	GACG	CTGCTG	CTGTGAA	CTGCTGGCTG	480
Qy	481	ACA	CCGGCT	GACCCAG	AGCTCC	ATCAGG	ACCCCT	GTGGT	CAG	ATCTCTG	540
Db	481	ACA	CCGGCT	GACCCAG	AGCTCC	ATCAGG	ACCCCT	GTGGT	CAG	ATCTCTG	540
Qy	541	TAT	CTCGGG	CACGCC	CAACAG	TGTG	ATCGCAG	CTAAC	CAG	CACCTCC	600
Db	541	TAT	CTCGGG	CACGCC	CAACAG	TGTG	ATCGCAG	CTAAC	CAG	CACCTCC	600
Qy	601	TC	CTGGT	GACAAG	CAATTA	AAGCTG	CTTGA	TAA	CAAG	CTGTG	660
Db	601	TC	CTGGT	GACAAG	CAATTA	AAGCTG	CTTGA	TAA	CAAG	CTGTG	660
Qy	661	AC	CTGGT	GACGGT	GTCA	ATCTCC	ACCTGG	GCAC	CTTA	TATGG	720
Db	661	AC	CTGGT	GACGGT	GTCA	ATCTCC	ACCTGG	GCAC	CTTA	TATGG	720
Qy	721	CT	GAGT	CC	CAGATCC	CGCTAT	TCCAT	GTG	CTCC	ACTGT	780
Db	721	CT	GAGT	CC	CAGATCC	CGCTAT	TCCAT	GTG	CTCC	ACTGT	780
Qy	781	CC	CTG	GAAGTCA	ATGCTG	TTCTT	CTCTG	CTGG	CA	CCCCAT	840
Db	781	CC	CTG	GAAGTCA	ATGCTG	TTCTT	CTCTG	CTGG	CA	CCCCAT	840
Qy	841	CC	ACCC	CTTTG	CTG	CC	AAAGG	ATG	GGGTAC	CGAGGG	900
Db	841	CC	ACCC	CTTTG	CTG	CC	AAAGG	ATG	GGGTAC	CGAGGG	900
Qy	901	T	CTCC	AG	CAGCTG	TTTG	ACTCT	CG	CTG	CTG	960
Db	901	T	CTCC	AG	CAGCTG	TTTG	ACTCT	CG	CTG	CTG	960
Qy	961	T	G	GACAT	CA	G	G	G	CAG	CTG	1020
Db	961	T	G	GACAT	CA	G	G	G	CAG	CTG	1020
Qy	1021	G	G	CT	AT	CC	G	G	G	G	1080
Db	1021	G	G	CT	AT	CC	G	G	G	G	1080
Qy	1081	G	G	CT	GG	G	G	C	CA	C	1140
Db	1081	G	G	CT	GG	G	G	C	CA	C	1140
Qy	1141	C	CT	CT	G	T	G	G	G	G	1200
Db	1141	C	CT	CT	G	T	G	G	G	G	1200
Qy	1201	A	T	G	G	T	A	G	A	G	1260
Db	1201	A	T	G	G	T	A	G	A	G	1260
Qy	1261	C	G	T	G	T	G	G	G	G	1320
Db	1261	C	G	T	G	T	G	G	G	G	1320
Qy	1321	C	A	G	A	T	C	A	G	A	1380
Db	1321	C	A	G	A	T	C	A	G	A	1380
Qy	1381	A	T	G	C	T	C	T	T	G	1440
Db	1381	A	T	G	C	T	C	T	T	G	1440
Qy	1441	C	T	G	A	T	C	T	T	A	1500
Db	1441	C	T	G	A	T	C	T	T	A	1500
Qy	1501	G	A	G	G	C	A	A	C	A	1560

1501	Db	GAGSCAAGCACCTGGGAGCGCTGAGAGTGGGCGAGCTCGCTCTCAGGCGAATTTCTCA	1560
1561	Qy	TTTCAAGCCACTGGGGAACCTGAGGCAAAACCATACTAGTCTATCTACCAACAAGCTGGAC	1620
1561	Db	TTTCAAGCCACTGGGGAACCTGAGGCAAAACCATACTAGTCTATCTACCAACAAGCTGGAC	1620
1621	Qy	TGCTAGCTGGGCTGTTTATCTTCCCTGAGTGCCTGGGTCTCCCTCCCTCACTCTTGCC	1680
1621	Db	TGCTTAGCTGGGCTGTTTATCTTCCCTGAGTGCCTGGGTCTCCCTCCCTCACTCTTGCC	1680
1681	Qy	CTTTCGGTTCCTCTCTCTCTCTCCCTCTTCCTCATCTCCCGGCTCTCTCTCTGC	1740
1681	Db	CTTTCGGTTCCTCTCTCTCTCTCCCTCTTCCTCATCTCCCGGCTCTCTCTCTGC	1740
1741	Qy	CCACCCCGAGGGGAGCAGACTGCTCCTCCAGGCTGTATAGACCTGCCCTCTTGCAATTA	1800
1741	Db	CCACCCCGAGGGGAGCAGACTGCTCCTCCAGGCTGTATAGACCTGCCCTCTTGCAATTA	1800
1801	Qy	AACAACCTCTCTTGAGCTGC	1820
1801	Db	AACAACCTCTCTTGAGCTGC	1820

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RESULT 9
US-10-201-853-497
  Sequence 497, Application US/10201853
  Publication No. US20040053358A1
  GENERAL INFORMATION:
  APPLICANT: Baker, Kevin P.
  APPLICANT: Chen, Jian
  APPLICANT: Desnoyers, Luc
  APPLICANT: Goddard, Audrey
  APPLICANT: Godowski, Paul J.
  APPLICANT: Gurney, Austin L.
  APPLICANT: Pan, James
  APPLICANT: Smith, Victoria
  APPLICANT: Watanabe, Colin K.
  APPLICANT: Wood, William I.
  APPLICANT: Zhang, Zemin
  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
  FILE REFERENCE: P3430RJC465
  CURRENT APPLICATION NUMBER: US/10/201,853
  CURRENT FILING DATE: 2002-07-23
  PRIOR APPLICATION NUMBER: 10/052586
  PRIOR FILING DATE: 2002-01-15
  PRIOR APPLICATION NUMBER: 60/059263
  PRIOR FILING DATE: 1997-09-18
  PRIOR APPLICATION NUMBER: 60/059266
  PRIOR FILING DATE: 1997-09-18
  PRIOR APPLICATION NUMBER: 60/062250
  PRIOR FILING DATE: 1997-10-17
  PRIOR APPLICATION NUMBER: 60/063120
  PRIOR FILING DATE: 1997-10-24
  PRIOR APPLICATION NUMBER: 60/063121
  PRIOR FILING DATE: 1997-10-24
  PRIOR APPLICATION NUMBER: 60/063486
  PRIOR FILING DATE: 1997-10-21
  PRIOR APPLICATION NUMBER: 60/063540
  PRIOR FILING DATE: 1997-10-28
  PRIOR APPLICATION NUMBER: 60/063541
  PRIOR FILING DATE: 1997-10-28
  PRIOR APPLICATION NUMBER: 60/063544
  PRIOR FILING DATE: 1997-10-28
  Prior Application data removed - See file wrapper or PALM.
  NUMBER OF SEQ ID NOS: 612
  SEQ ID NO 497
  LENGTH: 1820
  TYPE: DNA
  ORGANISM: Homo Sapien
US-10-201-853-497

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US-10-201-853-497

Query Match: 99.2%; Score 1816.8; DB 13; Length 1820;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1818; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 1 GCCTATAAAGTACCTCTCTGATCTGCTGCTCGGCGAGAGAGGCTACCTCTGGGCT 60

QY 61 GAGAGTTCACCTGCTCAGAAACACCTGAGCCACAGATCTCTGGGCGAGG 120  
DB 61 GAGAGTTCACCTGCTCAGAAACACCTGAGCCACAGATCTCTGGGCGAGG 120

QY 121 CAGCCATGGCTTGGGCAAGTGGTGGGCTGCTGCTGGGCACTGCTGCTGGTGG 180  
DB 121 CAGCCATGGCTTGGGCAAGTGGTGGGCTGCTGCTGGGCACTGCTGCTGGTGG 180

QY 181 GTGCTTCAGCCAGGCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
DB 181 GTGCTTCAGCCAGGCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240

QY 241 AAATGGGAAAGCCCTCTCAGCGGCGCTGCGAGGTCATCTGCTCAATTTCTGACT 300  
DB 241 AAATGGGAAAGCCCTCTCAGCGGCGCTGCGAGGTCATCTGCTCAATTTCTGACT 300

QY 301 GGAGTGGAGGCGCTTCAGCCACAGGATCGGATTCGATTCGATTCGATTCGATTC 360  
DB 301 GGAGTGGAGGCGCTTCAGCCACAGGATCGGATTCGATTCGATTCGATTCGATTC 360

QY 361 TCACCTGAAATTCATTTGCTGCTTTCGAGTGGGCTGCTGCTGCTGCTGCTGCTGCT 420  
DB 361 TCACCTGAAATTCATTTGCTGCTTTCGAGTGGGCTGCTGCTGCTGCTGCTGCTGCT 420

QY 421 TCAAGTCTTTGCGGCCCGAGAGCCCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 480  
DB 421 TCAAGTCTTTGCGGCCCGAGAGCCCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 480

QY 481 ACACCGCGTACCGAGCTCCATCAGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
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QY 541 TATTTCTGGGCCCGAGGCTTTCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 600  
DB 541 TATTTCTGGGCCCGAGGCTTTCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 600

QY 601 TCTGCTGAGAGGACATTAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660  
DB 601 TCTGCTGAGAGGACATTAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660

QY 661 ACTGCTGAGGCTGCTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720  
DB 661 ACTGCTGAGGCTGCTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720

QY 721 CTGAGTCCAGATCCGCTATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
DB 721 CTGAGTCCAGATCCGCTATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780

QY 781 CCTGAGTCAATGCTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840  
DB 781 CCTGAGTCAATGCTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840

QY 841 CCACCCCTTTGTTGCGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
DB 841 CCACCCCTTTGTTGCGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900

QY 901 TCTCCAGAGCTGTTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960  
DB 901 TCTCCAGAGCTGTTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960

QY 961 TGGACATCACAGGCGAGTGGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCG 1020  
DB 961 TGGACATCACAGGCGAGTGGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCG 1020

QY 1021 GGCTCATCCGGAGTGGCGCGCCAGTTCCTCCGAGGCCATGCTGCTGCTGCTGCTGCTGCT 1080

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QY 1081 GGCCTGGTGCACACCTGCTGGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140

DB 1081 GGCCTGGTGCACACCTGCTGGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140

QY 1141 CCTTCGTGAGGCTGCTGGCCACAGCTTCCAACTCGGCTTTCAGTCCCTCTCTCTCTCTCTCT 1200

DB 1141 CCTTCGTGAGGCTGCTGGCCACAGCTTCCAACTCGGCTTTCAGTCCCTCTCTCTCTCTCTCT 1200

QY 1201 ATGTGTAGTGAATTCAGACTCCAGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260

DB 1201 ATGTGTAGTGAATTCAGACTCCAGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260

QY 1261 CGTCTGCTGCTGGGAGTTCAGCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320

DB 1261 CGTCTGCTGCTGGGAGTTCAGCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320

QY 1321 CAGATCAGGTCGCGCACACTGATGGGCAACCGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380

DB 1321 CAGATCAGGTCGCGCACACTGATGGGCAACCGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380

QY 1381 ATGCTCTCTTGGCCATGGGAAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440

DB 1381 ATGCTCTCTTGGCCATGGGAAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440

QY 1441 CTGAGATCTTTGCTATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500

DB 1441 CTGAGATCTTTGCTATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500

QY 1501 GAGGCAAGACCACTGGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560

DB 1501 GAGGCAAGACCACTGGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560

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QY 1801 AACAACTTCTCTGAGCTGC 1820

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## RESULT 10

US-10-174-581-497

; Sequence 497, Application US/10174581

; Publication No. US20030017540A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

1 TITLE OF INVENTION: ACIDS ENCODING THE SAME  
2 FILE REFERENCE: P3430R1C41  
3 CURRENT APPLICATION NUMBER: US/1C/174,581  
4  
5 PRIOR FILING DATE: 2002-06-18  
6 PRIOR APPLICATION NUMBER: 10/052586  
7  
8 PRIOR FILING DATE: 2002-01-15  
9 PRIOR APPLICATION NUMBER: 60/059263  
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11 PRIOR FILING DATE: 1997-09-18  
12 PRIOR APPLICATION NUMBER: 60/059266  
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216 PRIOR APPLICATION NUMBER: 60/088212  
217  
218 PRIOR FILING DATE: 1998-06-05

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 37 PRIOR APPLICATION NUMBER: 60/089598  
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 39 PRIOR APPLICATION NUMBER: 60/089653

Query Match	99.2%;	Score 1816.8;	DB 13;	Length 1820;
Best Local Similarity	99.9%;	Prod. No. 0;		
Matches 1818;	Conservative	0;	Mismatches 2;	Indels 0;
Gaps	0;			
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DB	1	GCCTTATAAGTAGCCTCTGCATCTGCCTGCTCGCGGACAGAGGAGGCTACCTCGGGGCT	60	
QY	61	GAGAGTTTCACCTGTCTCAGGAACACACCTGAGCCCAACAGATCCTGTGGCAGCGGCCAGGG	120	
DB	61	GAGAGTTTCACCTGTCTCAGGAACACACCTGAGCCCAACAGATCCTGTGGCAGCGGCCAGGG	120	
QY	121	CAGCCATGGCTTTGGGCAAGTAGGCTGGCTGTGGCTGGCACTGCTGCTGCCCGTGGTCG	180	
DB	121	CAGCCATGGCTTTGGGCAAGTAGGCTGGCTGTGGCTGGCACTGCTGCTGCCCGTGGTCG	180	
QY	181	GTGCTCTCCAGCGCAGGACCGTGTCGGACTCAACAAGGCAGCATTCAGACTACGTGCTG	240	
DB	181	GTGCTCTCCAGCGCAGGACCGTGTCGGACTCAACAAGGCAGCATTCAGACTACGTGCTG	240	
QY	241	AAATTGGGAAGCCCTCTCCAGGGGCCCTGCAGGTCACTGTCCCTCATTTCTTGACT	300	
DB	241	AAATTGGGAAGCCCTCTCCAGGGGCCCTGCAGGTCACTGTCCCTCATTTCTTGACT	300	
QY	301	GGAGTGAGAGGCGCTTCAGCCCAACAGGATCCGGAATTCGAATGTCCATGTGCCCGGCC	360	
DB	301	GGAGTGAGAGGCGCTTCAGCCCAACAGGATCCGGAATTCGAATGTCCATGTGCCCGGCC	360	
QY	361	TCCACCTGAAATTCATGCTGGTTTCGGAGTCGGCTGTGGCAGCAGCTAAATTTACTT	420	
DB	361	TCCACCTGAAATTCATGCTGGTTTCGGAGTCGGCTGTGGCAGCAGCTAAATTTACTT	420	
QY	421	TCAGGTCTTTGCGGCCCAAGACCCCTGGAGCTGACGTGCTGTGGAACTCTCGGCTG	480	

Db	421	TCAAGGTCCTTTTGGCGCCCCAGAGCCCTTGAGCTGAOCTGCCTCTGGAACTGTCTGGCTG 480
QY	481	ACACC CGGTGACCCAGAGCTCATCAGAGCCCCTGTGGTCAAGCATCTCTGCCCTCTCT 540
Dd	481	ACACC CGGTGACCCAGAGCTCATCAGAGCCCCTGTGGTCAAGCATCTCTGCCCTCTCT 540
QY	541	TATTTCTCGGGCCACCGCCAAAGATTGTATGGCAGTAACAGCACCTCCACGCGTCTGCG 600
Dd	541	TATTTCTCGGGCCACCGCCAAAGATTGTATGGCAGTAACAGCACCTCCACGCGTCTGCG 600
QY	601	TCTGTGTGCAGAAGCACATAAAGCTGTCTTAGTAAACAAGCTGTGCTCTGAGCATCTCCA 660
Dd	601	TCTGTGTGCAGAAGCACATAAAGCTGTCTTAGTAAACAAGCTGTGCTCTGAGCATCTCCA 660
QY	661	ACCTGGTCAGGGTGTCAATGTCCACTCGGGCACCTTAATTGGCTCAACCCCGTGGGTC 720
Dd	661	ACCTGGTCAGGGTGTCAATGTCCACTCGGGCACCTTAATTGGCTCAACCCCGTGGGTC 720
QY	721	CTGAGTCCCGATCCGGCTATTTCATAGTGTAGTGTGCCCACTGTGTCAACAGTGACTACATT 780
Dd	721	CTGAGTCCCGATCCGGCTATTTCATAGTGTAGTGTGCCCACTGTGTCAACAGTGACTACATT 780
QY	781	CCCTCGAAGTCAATGCTGTCTCTCTCTGCTGGGCAAGCCCATCATCTGCTGCCACGGATG 840
Dd	781	CCCTCGAAGTCAATGCTGTCTCTCTCTGCTGGGCAAGCCCATCATCTGCTGCCACGGATG 840
QY	841	CCACCCTTTTGTGTGCCAAGCAATGGGTACCGAGGGCTCCATGGCCCAACCGTGGGCC 900
Dd	841	CCACCCTTTTGTGTGCCAAGCAATGGGTACCGAGGGCTCCATGGCCCAACCGTGGGCC 900
QY	901	TCTCCACGACGTGTTGACTCTGGCTCTGGCTCTGGCTCTGGCTCTGGCTCTGGCTCTGGCT 960
Dd	901	TCTCCACGACGTGTTGACTCTGGCTCTGGCTCTGGCTCTGGCTCTGGCTCTGGCTCTGGCT 960
QY	961	TGGACATCACAGGGCAGCTGAGGTGCGATGACAACTGCTGAAACACTCTGCTCTGGGCC 1020
Dd	961	TGGACATCACAGGGCAGCTGAGGTGCGATGACAACTGCTGAAACACTCTGCTCTGGGCC 1020
QY	1021	GCTCTATCCCGAGGTGCCCGCCAGTTTCCCGAGCCCATGCTCTGGTGTCTCAAGTGC 1080
Dd	1021	GCTCTATCCCGAGGTGCCCGCCAGTTTCCCGAGCCCATGCTCTGGTGTCTCAAGTGC 1080
QY	1081	GCTCGGTGCCACACTGTGGCCATGCTCCACACAAAACGCCACCTCGCGCTGCAGC 1140
Dd	1081	GCTCGGTGCCACACTGTGGCCATGCTCCACACAAAACGCCACCTCGCGCTGCAGC 1140
QY	1141	CCTTCGTGGAGTCTCGGCCACAGCTCCAACTCGGCTTTCCAGTCCCTCTTCTCCCTGG 1200
Dd	1141	CCTTCGTGGAGTCTCGGCCACAGCTCCAACTCGGCTTTCCAGTCCCTCTTCTCCCTGG 1200
QY	1201	ATGTGTAGTGAATCTGAGACTCCAGCTCTCTGTGTCGAAGGTGAGCTTCAGGGACCA 1260
Dd	1201	ATGTGTAGTGAATCTGAGACTCCAGCTCTCTGTGTCGAAGGTGAGCTTCAGGGACCA 1260
QY	1261	CGTCTGTGTGGGGATGTCCAGCTCAOGTGGCTCTCTCAAACGTGGGCTTCATTGATA 1320
Dd	1261	CGTCTGTGTGGGGATGTCCAGCTCAOGTGGCTCTCTCAAACGTGGGCTTCATTGATA 1320
QY	1321	CAGATCAGGTGCCACACTGATGGGCAACGGTTTTTGGAGAGCCCTGCTGGACCATCTCA 1380
Dd	1321	CAGATCAGGTGCCACACTGATGGGCAACGGTTTTTGGAGAGCCCTGCTGGACCATCTCA 1380
QY	1381	ATGCTCTCTGGCCATGGGAATTGCCCTCCCTGGTGTGGTCAACCTCCACTATGTCCGCC 1440
Dd	1381	ATGCTCTCTGGCCATGGGAATTGCCCTCCCTGGTGTGGTCAACCTCCACTATGTTCGCC 1440
QY	1441	CTGAGATCTTTGTCTATGAGGCTACGTGGTGATATCCAGTGGACTCTTTCTACCAAGCT 1500
Dd	1441	CTGAGATCTTTGTCTATGAGGCTACGTGGTGATATCCAGTGGACTCTTTCTACCAAGCT 1500
QY	1501	GAGGCAAGACCACTGGAGGCTGTGAGGTGGGCGAGTCTGCTGTCTCAGCGAATTTCTCA 1560





Db 1321 CAGATCAAGTGGGCACTGATGGGACCGCTTTTGTGAGAGCCCTGCTGGACCATCTCA 1380  
QY 1381 ATGCTCTCTTGGCCATGGGAATTGCCCTCCCTGCTGGTGGTCAACCTCCATCTATCTGCC 1440  
Db 1381 ACCTCTCTTGGCCATGGGAATTGCCCTCCCTGCTGGTGGTCAACCTCCATCTATCTGCC 1440  
QY 1441 CTGAGATCTTTGTCTATGAGGGCTACGCTGGTGGTATCCAGTGGACTCTTCTACAGAGCT 1500  
Db 1441 CTGAGATCTTTGTCTATGAGGGCTACGCTGGTGGTATCCAGTGGACTCTTCTACAGAGCT 1500  
QY 1501 GAGCAAGACCACTGGGAGGCTGAGAGTGGGCGGCTGCTGCTCAGGCGAATTTCTCA 1560  
Db 1501 GAGCAAGACCACTGGGAGGCTGAGAGTGGGCGGCTGCTGCTCAGGCGAATTTCTCA 1560  
QY 1561 TTTCAAGCCACTGGGGAATCTAGGCAAAACCATCTAGTCTATCAACCAAGCTGGAC 1620  
Db 1561 TTTCAAGCCACTGGGGAATCTAGGCAAAACCATCTAGTCTATCAACCAAGCTGGAC 1620  
QY 1621 TGCTAGCTGGGCTGTTTATCTCCCTGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680  
Db 1621 TGCTAGCTGGGCTGTTTATCTCCCTGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680  
QY 1681 CTCTCCCT 1740  
Db 1681 CTCTCCCT 1740  
QY 1741 CCACCCCGAGGGGAGGAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1800  
Db 1741 CCACCCCGAGGGGAGGAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1800  
QY 1801 AACCACTCTCTGAGCTGC 1820  
Db 1801 AACCACTCTCTGAGCTGC 1820

## RESULT 12

US-10-176-749-497  
; Sequence 497, Application US/10176749  
; Publication No. US20030017542A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Guiney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P343R1C76  
; CURRENT APPLICATION NUMBER: US/10/176, 749  
; CURRENT FILING DATE: 2002-06-20  
; Prior application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 497  
; LENGTH: 1820  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-176-749-497

Query Match 99.2%; Score 1816.8; DB 13; Length 1820;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1818; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCTTATAAGTAGCTCTGATCTGCTGCTCGGCGAGGAGGGCTACCTGGGGCT 60  
Db 1 GCCTTATAAGTAGCTCTGATCTGCTGCTCGGCGAGGAGGGCTACCTGGGGCT 60  
QY 61 GAGAGTTCACTGTCTCAGGAACCACTGAGCCCAAGATCTCTGTGGGCGAGGGCCAGGG 120

Db 61 GAGAGTTCACTGTCTCAGGAACCACTGAGCCCAAGATCTCTGTGGGCGAGGGCCAGGG 120  
QY 121 CAGGCATGGCTTGGGCAAGTAGGCTGGGCTGCTGTGGGCACTGCTGCTGCTGCTGCTGCTG 180  
Db 121 CAGGCATGGCTTGGGCAAGTAGGCTGGGCTGCTGTGGGCACTGCTGCTGCTGCTGCTGCTG 180  
QY 181 GTGCTCTCAGCCAGGCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
Db 181 GTGCTCTCAGCCAGGCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
QY 241 AAATGGGAAAGCCCTCTCCAGCGGCCCCTGCAAGGCTCACTGCTCCCTCACTTCTGAGCT 300  
Db 241 AAATGGGAAAGCCCTCTCCAGCGGCCCCTGCAAGGCTCACTGCTCCCTCACTTCTGAGCT 300  
QY 301 GGAGTGGAGAGGCGCTCTCAGGCCCAAGGATCCGGATCTGMAATGTCATGTGCCCCGCC 360  
Db 301 GGAGTGGAGAGGCGCTCTCAGGCCCAAGGATCCGGATCTGMAATGTCATGTGCCCCGCC 360  
QY 361 TCACCTCTGAAATTCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420  
Db 361 TCACCTCTGAAATTCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420  
QY 421 TCAAGTCTTTTCGGGCCCCAGAGCCCTGAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTG 480  
Db 421 TCAAGTCTTTTCGGGCCCCAGAGCCCTGAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTG 480  
QY 481 ACACCCGCTGACCCAGAGCTCCATCAGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
Db 481 ACACCCGCTGACCCAGAGCTCCATCAGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
QY 541 TATTTCTGGGCCACGCCAAGAGTTTGTGAGGAGTAAACAGCACTCCACGCGCTGCTGG 600  
Db 541 TATTTCTGGGCCACGCCAAGAGTTTGTGAGGAGTAAACAGCACTCCACGCGCTGCTGG 600  
QY 601 TCTGCTGAGAGAGCACTTAAAGCTGCTTGTAGTAAACAGCTGTGCTGCTGAGCATCTCCA 660  
Db 601 TCTGCTGAGAGAGCACTTAAAGCTGCTTGTAGTAAACAGCTGTGCTGCTGAGCATCTCCA 660  
QY 661 ACTGCTGAGAGGCTGCAATGCTCCACTGGGCACTTAAATGAGCTGCTGCTGCTGCTGCTG 720  
Db 661 ACTGCTGAGAGGCTGCAATGCTCCACTGGGCACTTAAATGAGCTGCTGCTGCTGCTGCTG 720  
QY 721 CTGAGTCCAGATCCGCTATTCATGCTGAGTGGCCCACTGTCACAGAGTGAATACATTT 780  
Db 721 CTGAGTCCAGATCCGCTATTCATGCTGAGTGGCCCACTGTCACAGAGTGAATACATTT 780  
QY 781 CCTGGAAGTCAATGCTGCTCTCTCTGCTGAGGCAAGCCCAATCATCTGCTGCTGCTGCTG 840  
Db 781 CCTGGAAGTCAATGCTGCTCTCTCTGCTGAGGCAAGCCCAATCATCTGCTGCTGCTGCTG 840  
QY 841 CCACCCCTTTGCTGCTGCAAGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
Db 841 CCACCCCTTTGCTGCTGCAAGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
QY 901 TCTCCAGAGCTGTTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960  
Db 901 TCTCCAGAGCTGTTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960  
QY 961 TGGACATCAGAGGCGAGCTGAGTGGATGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020  
Db 961 TGGACATCAGAGGCGAGCTGAGTGGATGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020  
QY 1021 GGCTCATCCCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080  
Db 1021 GGCTCATCCCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080  
QY 1081 GGCTGGGTGCCACACTGTGGCCATGCTCCACAAACCAACGCCACCCCTGCGGCTGCAGC 1140  
Db 1081 GGCTGGGTGCCACACTGTGGCCATGCTCCACAAACCAACGCCACCCCTGCGGCTGCAGC 1140  
QY 1141 CCTTCTGGAGGTTCTTGGCCACAGGCTGCAACTCGGCTTTTCCAGTCCCTCTCTCTCTCTG 1200



Db 1141 CCTCTGTGGAGGCTCTGGCCACAGCCTCCAACTGGCTTTCCAGTCCCTCTCTCCCTGG 1200  
Qy 1201 ATGTGGTAGTGAACCTGAGACTCCAGCTCTCTGTGTCCAAAGTGAAGCTTCAGGGGACCA 1260  
Db 1201 ATGTGGTAGTGAACCTGAGACTCCAGCTCTCTGTGTCCAAAGTGAAGCTTCAGGGGACCA 1260  
Qy 1261 CGTCTGTGCTGGGGGATGTCCAGTCCAGCTACGGTGGCTCTCTCAACGTGGGCTTCATTGATA 1320  
Db 1261 CGTCTGTGCTGGGGGATGTCCAGTCCAGTACGGTGGCTCTCTCAACGTGGGCTTCATTGATA 1320  
Qy 1321 CAGATCAGGTGGCCACACTGATGGGACCCGTTTGTGAGAGCCCTCTCTGACCATCTCA 1380  
Db 1321 CAGATCAGGTGGCCACACTGATGGGACCCGTTTGTGAGAGCCCTCTCTGACCATCTCA 1380  
Qy 1381 ATGCTCTCTGGCCATGGGAATGGCCCTCCCTGGTGTGGTCAACCTCCACTATGTGGCCC 1440  
Db 1381 ATGCTCTCTGGCCATGGGAATGGCCCTCCCTGGTGTGGTCAACCTCCACTATGTGGCCC 1440  
Qy 1441 CTGAGATCTTTGTCTATGAGGGCTAGTGTGATATCCAGTGAAGCTTTCTACAGAGCT 1500  
Db 1441 CTGAGATCTTTGTCTATGAGGGCTAGTGTGATATCCAGTGAAGCTTTCTACAGAGCT 1500  
Qy 1501 GAGGCAAGCACTGGGAGGCTGAGGTGGGCGAGCTCGCTCTCAGGGGAATTTCTCA 1560  
Db 1501 GAGGCAAGCACTGGGAGGCTGAGGTGGGCGAGCTCGCTCTCAGGGGAATTTCTCA 1560  
Qy 1561 TTTCAAGCCACTGGGAAACTGAGGCAAAACCATATCTAGTATCATCAACCAAGCTGGAC 1620  
Db 1561 TTTCAAGCCACTGGGAAACTGAGGCAAAACCATATCTAGTATCATCAACCAAGCTGGAC 1620  
Qy 1621 TGCTTAGTGGGCTGTTTATCTCTCTCCCTGAGTGGCTGCTCCCTCCCTCTCTGCTGC 1680  
Db 1621 TGCTTAGTGGGCTGTTTATCTCTCTCCCTGAGTGGCTGCTCCCTCCCTCTCTGCTGC 1680  
Qy 1681 CTTTCCCTCTCCCT 1740  
Db 1681 CTTTCCCT 1740  
Qy 1741 CCCACCCAGGGGGAGCAGACTGCTCTCCAGGTGTATAGACTGCTCCCTCTCTGCAATTA 1800  
Db 1741 CCCACCCAGGGGGAGCAGACTGCTCTCCAGGTGTATAGACTGCTCCCTCTCTGCAATTA 1800  
Qy 1801 AACCACTCTCTTGAGCTGC 1820  
Db 1801 AACCACTCTCTTGAGCTGC 1820

## RESULT 13

US-10-176-914-497  
; Sequence 497, Application US/10176914  
; Publication No. US20030017543A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3430R1C83  
; CURRENT APPLICATION NUMBER: US/10/176,914  
; CURRENT FILING DATE: 2002-06-20  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 497  
; LENGTH: 1820  
; TYPE: DNA

; ORGANISM: Homo Sapien  
US-10-176-914-497

Query Match  
Best Local Similarity 99.2%; Score 1816.8; DB 13; Length 1820;  
Matches 1818; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCCTTATAAGTAGCTCTGCTGCTGGGAGAGGGGTACCTGGGGCT 60  
Db 1 GCCTTATAAGTAGCTCTGCTGCTGGGAGAGGGGTACCTGGGGCT 60  
Qy 61 GAGAGTTCACCTGTCTCAGGAACCACTGAGCCACAGATCCTGTGGCAGGCGCCAGG 120  
Db 61 GAGAGTTCACCTGTCTCAGGAACCACTGAGCCACAGATCCTGTGGCAGGCGCCAGG 120  
Qy 121 CAGCCATGGCTTGGGCAAGTAGGCTGGGCTGTGCTGGCACTGCTGTGCCCTGGTGG 180  
Db 121 CAGCCATGGCTTGGGCAAGTAGGCTGGGCTGTGCTGGCACTGCTGTGCCCTGGTGG 180  
Qy 181 GTCCCTCCAGCCAGGCAAGTAGGCTGGGCTGTGCTGGCACTGCTGTGCCCTGGTGG 240  
Db 181 GTCCCTCCAGCCAGGCAAGTAGGCTGGGCTGTGCTGGCACTGCTGTGCCCTGGTGG 240  
Qy 241 AATTTGGGAAGCCCTCTCTCAGGCGGCGCTGAGGATCCGATTCGATTCCTGACT 300  
Db 241 AATTTGGGAAGCCCTCTCTCAGGCGGCGCTGAGGATCCGATTCGATTCCTGACT 300  
Qy 301 GGAGTGGAGAGGCGCTTCAGCCACAGGATCCGATTCGATTCCTGACTTCCTGACT 360  
Db 301 GGAGTGGAGAGGCGCTTCAGCCACAGGATCCGATTCGATTCCTGACTTCCTGACT 360  
Qy 361 TCCACTGAATTCATGCTGCTGGTTCGAGTGGCGCTGCTGGCACTGCTGCTGACTT 420  
Db 361 TCCACTGAATTCATGCTGCTGGTTCGAGTGGCGCTGCTGGCACTGCTGCTGACTT 420  
Qy 421 TCAAGTCTTTTCGCGCCCGCAGAGCCCTGAGTGGCGCTGCTGGCACTGCTGCTGACT 480  
Db 421 TCAAGTCTTTTCGCGCCCGCAGAGCCCTGAGTGGCGCTGCTGGCACTGCTGCTGACT 480  
Qy 481 ACACCGGCTGACCCAGAGCTCCATCAGGACCCCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
Db 481 ACACCGGCTGACCCAGAGCTCCATCAGGACCCCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
Qy 541 TATTTCTCGGGCCACCCAGAGCTTTGATGGCAGTTCAGGACCTCCCGAGGCTGCTGG 600  
Db 541 TATTTCTCGGGCCACCCAGAGCTTTGATGGCAGTTCAGGACCTCCCGAGGCTGCTGG 600  
Qy 601 TCCTGGTGCAGAAAGCACATTAAGCTGCTTTCAGTAAACAGCTGTGCTGCTGCTGCTGCT 660  
Db 601 TCCTGGTGCAGAAAGCACATTAAGCTGCTTTCAGTAAACAGCTGTGCTGCTGCTGCTGCT 660  
Qy 661 ACCTGGTGCAGGGTGTCAATGTCCACCTGGGCACTTAAATGGCCCTCAACCCGCTGG 720  
Db 661 ACCTGGTGCAGGGTGTCAATGTCCACCTGGGCACTTAAATGGCCCTCAACCCGCTGG 720  
Qy 721 CTGAGTCCAGATCCGCTTATTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
Db 721 CTGAGTCCAGATCCGCTTATTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
Qy 781 CCCTGGAAAGTCAATGCTGCTTCTCTCTGCTGGGCAAGCCCATCATCTGCTGCTGCTGCT 840  
Db 781 CCCTGGAAAGTCAATGCTGCTTCTCTCTGCTGGGCAAGCCCATCATCTGCTGCTGCTGCT 840  
Qy 841 CCACCCCTTTTGTGTTCCCAAGGCAATGGGTACCCGAGGCTCCATGGCCACCCGCTGG 900  
Db 841 CCACCCCTTTTGTGTTCCCAAGGCAATGGGTACCCGAGGCTCCATGGCCACCCGCTGG 900  
Qy 901 TCTCCAGAGAGCTTTTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
Db 901 TCTCCAGAGAGCTTTTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
Qy 961 TGGACATCAAGGCGAGCTGAGGTGGATGACCAACCTGCTGAAACACCTGCTGCTGCTGCT 1020  
Db 961 TGGACATCAAGGCGAGCTGAGGTGGATGACCAACCTGCTGAAACACCTGCTGCTGCTGCT 1020

D <sub>b</sub>	961	TGGACATCAAGGCGCAGTGAGGTGCAGTGAACAACCCTGCTGAACACACTCTGCTCTGGGCC	1020
Q <sub>y</sub>	1021	GGCTCATCCCGAGGTGGCCCGCCAGATTCCCAGAGCCCATGCCCTGTGTGTCCTCAAAGTGCC	1080
D <sub>b</sub>	1021	GGCTCATCCCGAGGTGGCCCGCCAGATTCCCAGAGCCCATGCCCTGTGTGTCCTCAAAGTGCC	1080
Q <sub>y</sub>	1081	GCGTGGGTGCCACACCTGTGGCCATGTCCACACAACAAAGCACCCCTCGCGCTCGAGC	1140
D <sub>b</sub>	1081	GCGTGGGTGCCACACCTGTGGCCATGTCCACACAACAAAGCACCCCTCGCGCTCGAGC	1140
Q <sub>y</sub>	1141	CCTTTCTGTGAGAGTCCCTGGCCACAGCCTCCAATCTGGCTTTCCAGTCCCTCTTCTCCCTGG	1200
D <sub>b</sub>	1141	CCTTTCTGTGAGAGTCCCTGGCCACAGCCTCCAATCTGGCTTTCCAGTCCCTCTTCTCCCTGG	1200
Q <sub>y</sub>	1201	ATGTGTAGTAGAATTGAGACTCCAGCTCTCTGTGTCCAAGGTGAAGCTTCAGGGACCA	1260
D <sub>b</sub>	1201	ATGTGTAGTAGAATTGAGACTCCAGCTCTCTGTGTCCAAGGTGAAGCTTCAGGGACCA	1260
Q <sub>y</sub>	1261	CGTCTGTGCTGGGGATGTCCAGCTCAGGTGGCTTCTCCACAGTGGGTTCAITTAATA	1320
D <sub>b</sub>	1261	CGTCTGTGCTGGGGATGTCCAGCTCAGGTGGCTTCTCCACAGTGGGTTCAITTAATA	1320
Q <sub>y</sub>	1321	CAGATCAGSTGCGCACACTGATGGGCACCGTTTTTGTAGAAGCCCCCTGCTGGACCACTCTCA	1380
D <sub>b</sub>	1321	CAGATCAGSTGCGCACACTGATGGGCACCGTTTTTGTAGAAGCCCCCTGCTGGACCACTCTCA	1380
Q <sub>y</sub>	1381	ATGCTCTGTGGCCATGGGNATGTGCCCTCGTGGTGTGTCAACTCCACTATGTGGGCC	1440
D <sub>b</sub>	1381	ATGCTCTGTGGCCATGGGNATGTGCCCTCGTGGTGTGTCAACTCCACTATGTGGGCC	1440
Q <sub>y</sub>	1441	CTGAGATCTTTGTCTATGAGGGCTACGTGGTGATATCCAGTGGACTCTTCTACCAAGGCT	1500
D <sub>b</sub>	1441	CTGAGATCTTTGTCTATGAGGGCTACGTGGTGATATCCAGTGGACTCTTCTACCAAGGCT	1500
Q <sub>y</sub>	1501	GAGGCAAGHCCACTGGGAGGCTGTGAGTGGGCCAGCTCGCTGCTCAGCGAATTCTCA	1560
D <sub>b</sub>	1501	GAGGCAAGAACCTATGGGAGGCTGTGAGTGGGCCAGCTCGCTGCTCAGCGAATTCTCA	1560
Q <sub>y</sub>	1561	TTTCAAGCCACTGGGGNAACTGAGGCAAAACCATATTAGTTCATCACCAACAGCTGSHC	1620
D <sub>b</sub>	1561	TTTCAAGCCACTGGGGNAACTGAGGCAAAACCATATTAGTTCATCACCAACAGCTGSHC	1620
Q <sub>y</sub>	1621	TGCTIAGCTGGGCTGTTFATCTTCCTTGAGTSCTGGGTCTCCCTCCCTCACTCTGCCC	1680
D <sub>b</sub>	1621	TGCTIAGCTGGGCTGTTFATCTTCCTTGAGTSCTGGGTCTCCCTCCCTCACTCTGCCC	1680
Q <sub>y</sub>	1681	CTTTCCCTTCCTCTCTCTCTTCTCCCTGCTTCTCCCTCATCTCCCCCTCTTCTCTGTC	1740
D <sub>b</sub>	1681	CTTTCCCTTCCTCTCTCTCTTCTCCCTGCTTCTCCCTCATCTCCCCCTCTTCTCTGTC	1740
Q <sub>y</sub>	1741	CCACCCAGGGGGAGCAGACTGCTCCTCCAGGSTGTATAGACTGCGGCTCTTTGCATT	1800
D <sub>b</sub>	1741	CCACCCAGGGGGAGCAGACTGCTCCTCCAGGSTGTATAGACTGCGGCTCTTTGCATT	1800
Q <sub>y</sub>	1801	AACAACTCTCTTGAGTGC	1820
D <sub>b</sub>	1801	AACAACTCTCTTGAGTGC	1820

RESULT 14

RESOLI 14  
US-10-176-915-497

: Sequence 497, Application US/10176915

Publication No. US20030017544A1

; GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul

APPLICANT: Gurney, Austin L

APPLICANT: Pan, James

APPLICANT: Smith, Victoria

APPLICANT: Watanabe, Colin K.

```

; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPT
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C110
; CURRENT APPLICATION NUMBER: US/10/176,915
; CURRENT FILING DATE: 2002-06-21
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 497
; LENGTH: 1820
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-915-497

```

Query Match 99.2%; Score 1816.8; DB 13; Length 1820;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1818; Conservative 0; Mismatches 2; Indels 0;

QY	1	GCCTTATAAGTAGCCCTCTGCATCTGCCTCGGCGCAGAGAGGGCTACCCCTGGGGCT	60
Db	1	GCCTTATAAGTAGCCCTCTGCATCTGCCTCGGCGCAGAGAGGGCTACCCCTGGGGCT	60
QY	61	GAGAGTTACACCTGTCTCAGGAACCACTGAGGCCACAGATCCCTGTGGGCGAGGCCCAGGG	120
Db	61	GAGAGTTACACCTGTCTCAGGAACCACTGAGGCCACAGATCCCTGTGGGCGAGGCCCAGGG	120
QY	121	CAGCCATGCTTTGGGCAAGTAGGCTGGGCGCTGCTGCGCACATGCTGCTCCCGTGGTCG	180
Db	121	CAGCCATGCTTTGGGCAAGTAGGCTGGGCGCTGCTGCGCACATGCTGCTCCCGTGGTCG	180
QY	181	GTGCTCTCACGCCGACGACCGGTGCTCCGACTCAACAGGCAGCATTTGAGCTAGTGCTCG	240
Db	181	GTGCTCTCACGCCGACGACCGGTGCTCCGACTCAACAGGCAGCATTTGAGCTAGTGCTCG	240
QY	241	AAATTGGGAAAGCCCTCTCCAGCGGGCCCTGGAGTCACTGTCCTCAATTCTCGGACT	300
Db	241	AAATTGGGAAAGCCCTCTCCAGCGGGCCCTGGAGTCACTGTCCTCAATTCTCGGACT	300
QY	301	GGAGTGGAGAGCGGCTTCAGCCACACAGATCCGGATCTCGAATGCCATGTGCCCGCC	360
Db	301	GGAGTGGAGAGCGGCTTCAGCCACACAGATCCGGATCTCGAATGCCATGTGCCCGCC	360
QY	361	TCCACTGAAATTCATCTGCTTTGGAGTGGCGCTGCTGGCAGCAGCTAAATTTACTT	420
Db	361	TCCACTGAAATTCATCTGCTTTGGAGTGGCGCTGCTGGCAGCAGCTAAATTTACTT	420
QY	421	TCAAGTCTTTTGGGCCCCAGAGCCCTGGAGCTGACGCTGCTGTGAACTGCTGGCTG	480
Db	421	TCAAGTCTTTTGGGCCCCAGAGCCCTGGAGCTGACGCTGCTGTGAACTGCTGGCTG	480
QY	481	ACACCGCGTGACCCAGAGCTCCATCAGSACCCCTGTGGTCAAGATCTCTGCGCTCTT	540
Db	481	ACACCGCGTGACCCAGAGCTCCATCAGSACCCCTGTGGTCAAGATCTCTGCGCTCTT	540
QY	541	TATTCTCGGCGCACCCACAGATTTGATGGCAGTAAACAGCACTCCACCGCTGCTGG	600
Db	541	TATTCTCGGCGCACCCACAGATTTGATGGCAGTAAACAGCACTCCACCGCTGCTGG	600
QY	601	TCCTGTGTCAGAGCACATTAAAGCTGTCTTGAGTAAACAAGCTGTGCTCGAGCATCTCCA	660
Db	601	TCCTGTGTCAGAGCACATTAAAGCTGTCTTGAGTAAACAAGCTGTGCTCGAGCATCTCCA	660
QY	661	ACCTGTGTCAGGGTGTCATGTCACCTGGGCACTTAATTTGGCGCTCAACCCGTTGGTC	720
Db	661	ACCTGTGTCAGGGTGTCATGTCACCTGGGCACTTAATTTGGCGCTCAACCCGTTGGTC	720
QY	721	CTGAGTCCCAGATCCCGCTATTTCATGTCAGTGTGCCACTGTCCACAGTCACTACATTT	780
Db	721	CTGAGTCCCAGATCCCGCTATTTCATGTCAGTGTGCCACTGTCCACAGTCACTACATTT	780
QY	781	CCTTGAAGTCAATGCTGTTCTCTTCTGCTGGGCAAGCCCATCATCTGTCGCCAGGATG	840



Db 601 TCCTGTGAGAGACATTAAGCTGCTTGAATAACAAGCTGTGCTGAGCATCTCCA 660  
Qy 661 AACTGTGAGAGTGTCAATATGCTCACTGGGACCTTAATGCGCTCAACCCGGTGGTC 720  
Db 661 AACTGTGAGAGTGTCAATATGCTCACTGGGACCTTAATGCGCTCAACCCGGTGGTC 720  
Qy 721 CTGAGTCCAGATCCGCTATTCATGCTCAGTGTGCCCACTGTCAACAGTGAATCAATTT 780  
Db 721 CTGAGTCCAGATCCGCTATTCATGCTCAGTGTGCCCACTGTCAACAGTGAATCAATTT 780  
Qy 781 CCCTGGAGTCAATGCTGTCTCTTCCTGCTGGGCAAGCCCATCATCTCCCTCCAGGATG 840  
Db 781 CCCTGGAGTCAATGCTGTCTCTTCCTGCTGGGCAAGCCCATCATCTCCCTCCAGGATG 840  
Qy 841 CCACCCCTTTTGTGTGCCAAGCATGTGCGGTACCGAGGGCTCCATGGCCACCGTGGGCC 900  
Db 841 CCACCCCTTTTGTGTGCCAAGCATGTGCGGTACCGAGGGCTCCATGGCCACCGTGGGCC 900  
Qy 901 TCTCCAGAGCTGTGTTGACTCTGGGCTCTCTGCTGTGAGAGGCCGGTGGCTCAACC 960  
Db 901 TCTCCAGAGCTGTGTTGACTCTGGGCTCTCTGCTGTGAGAGGCCGGTGGCTCAACC 960  
Qy 961 TGGACATCAGAGGAGCTGAGTGGATGATGATCAAACTGCTGAACACTCTGCTGAGGCT 1020  
Db 961 TGGACATCAGAGGAGCTGAGTGGATGATGATCAAACTGCTGAGGCTCTGCTGAGGCT 1020  
Qy 1021 GGCCTCATCCCGAGGTGGCCGCCAGTTTCCCGAGCCCATGCTGTGTGGTGTCAAGGTGC 1080  
Db 1021 GGCCTCATCCCGAGGTGGCCGCCAGTTTCCCGAGCCCATGCTGTGTGGTGTCAAGGTGC 1080  
Qy 1081 GGCCTGGTGCACACCTGTGGCCATGCTCCACAAACCCACCCCTGGCGCTGCAGC 1140  
Db 1081 GGCCTGGTGCACACCTGTGGCCATGCTCCACAAACCCACCCCTGGCGCTGCAGC 1140  
Qy 1141 CCTTCGTGGAGTCTCTGGCCAGAGCTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGT 1200  
Db 1141 CCTTCGTGGAGTCTCTGGCCAGAGCTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGT 1200  
Qy 1201 ATGTGGTGTGAGTGTGAGCTCCAGCTCTCTGTGTCCAAAGGTGAAGCTTCAGGGGACCA 1260  
Db 1201 ATGTGGTGTGAGTGTGAGCTCCAGCTCTCTGTGTCCAAAGGTGAAGCTTCAGGGGACCA 1260  
Qy 1261 CGTCTGTGCTGGGAGTGTGAGCTCCAGCTCCAGTGGGCTCTCTCAACCTGGGCTTCATTGATA 1320  
Db 1261 CGTCTGTGCTGGGAGTGTGAGCTCCAGCTCCAGTGGGCTCTCTCAACCTGGGCTTCATTGATA 1320  
Qy 1321 CAGATCAGGTGGACACTGATGGGACCGTTTTTGAAGAGCCCTGTGGACCATCTCA 1380  
Db 1321 CAGATCAGGTGGACACTGATGGGACCGTTTTTGAAGAGCCCTGTGGACCATCTCA 1380  
Qy 1381 ATGCTCTCTTGGCCATGGGAATGCGCTCCCTGGTGTGTGATCAACCTCCACTATGTGCGCC 1440  
Db 1381 ATGCTCTCTTGGCCATGGGAATGCGCTCCCTGGTGTGTGATCAACCTCCACTATGTGCGCC 1440  
Qy 1441 CTGAGTCTTGTCTATGAGGCTACGTGGTGTGATATCCAGTGGACTCTTCTACAGAGCT 1500  
Db 1441 CTGAGTCTTGTCTATGAGGCTACGTGGTGTGATATCCAGTGGACTCTTCTACAGAGCT 1500  
Qy 1501 GAGGCAAGACCTGGGAGGCTGAGAGTGGGCCAGCTCGCTGCTCAGGCGAATTTCTCA 1560  
Db 1501 GAGGCAAGACCTGGGAGGCTGAGAGTGGGCCAGCTCGCTGCTCAGGCGAATTTCTCA 1560  
Qy 1561 TTTCAAGCACTGGGAAACTGAGCAAAACCATATCTAGTCAATCAACCAAGCTGGAC 1620  
Db 1561 TTTCAAGCACTGGGAAACTGAGCAAAACCATATCTAGTCAATCAACCAAGCTGGAC 1620  
Qy 1621 TGCTTAGCTGGGCTCTTTATCTTCCCTGAGTGGCTGGGTCTCCCTCCCTCACTTCTGCC 1680  
Db 1621 TGCTTAGCTGGGCTCTTTATCTTCCCTGAGTGGCTGGGTCTCCCTCCCTCACTTCTGCC 1680  
Qy 1681 CTTTCCCTTCTCCCTGC 1740  
Db 1681 CTTTCCCTTCTCCCTGC 1740

Qy 1741 CCACCCCGAGGGGAGCAGCTGCTCTCCCTCCAGGCTGTATAGACCTGCCCTCTTGCATTA 1800  
Db 1741 CCACCCCGAGGGGAGCAGCTGCTCTCTCCCTCCAGGCTGTATAGACCTGCCCTCTTGCATTA 1800  
Qy 1801 AACAACTTCTCTTGTAGCTGC 1820  
Db 1801 AACAACTTCTCTTGTAGCTGC 1820

Search completed: June 30, 2004, 03:29:54  
Job time : 1157 secs

GenCore version: 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OK protein - protein search, using sw model

Run on: June 29, 2004, 10:54:39 ; Search time 59 seconds  
(without alignments)  
2193.335 Million cell updates/sec

Title: US-10-069-034-28

Perfect score: 2265

Sequence: 1 YAWASRLGLLALLPVVGA.....PEIFVGYGVWISSGLFYQS 458

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_29Jan04.\*

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2265	100.0	458	4 AAB74722	Aab74722 Human mem
2	2265	100.0	458	4 ABB08889	Abb08889 Human EPI
3	2265	100.0	458	4 AAU14479	Aau14479 Human cov
4	2265	100.0	458	4 AAU14243	Aau14243 Human cov
5	2265	100.0	458	5 AAU09947	Aau09947 Human (ne
6	2265	100.0	458	7 ADE85847	Ade85847 Human ant
7	2260	99.8	458	4 AAU29272	Aau29272 Human PRO
8	2260	99.8	458	4 ABB08888	Abb08888 Human EPI
9	2260	99.8	458	5 ABB84977	Abb84977 Human PRO
10	2260	99.8	458	5 ABB95583	Abb95583 Human ang
11	2260	99.8	458	6 ABU58648	Abu58648 Human PRO
12	2260	99.8	458	6 ABU88196	Abu88196 Novel hum
13	2260	99.8	458	6 ABU84511	Abu84511 Human sec
14	2260	99.8	458	6 ABR66385	Abr66385 Human sec
15	2260	99.8	458	6 ABR65775	Abr65775 Human sec
16	2260	99.8	458	6 ABU99715	Abu99715 Human sec
17	2260	99.8	458	6 ABU82954	Abu82954 Human PRO
18	2260	99.8	458	6 ABU90075	Abu90075 Novel hum
19	2260	99.8	458	6 ABR68324	Abr68324 Human sec
20	2260	99.8	458	6 ABU96377	Abu96377 Novel hum
21	2260	99.8	458	6 ABU92808	Abu92808 Human sec
22	2260	99.8	458	6 ABO08885	Abu08885 Human sec
23	2260	99.8	458	6 ABO02937	Abu02937 Human sec
24	2260	99.8	458	6 ABR75091	Abr75091 Human sec
25	2260	99.8	458	6 ABR94853	Abr94853 Human sec

## ALIGNMENTS

### RESULT 1

AAB74722

ID AAB74722 standard; protein; 458 AA.

XX AC AAB74722;

XX XX 12-JUN-2001 (first entry)

DE Human membrane associated protein MEMAP-28.

XX KW Human; membrane associated protein; MEMAP; diagnosis; cytostatic;  
KW antiinflammatory; anticonvulsant; immunosuppressive; antidiarrheic;  
KW antiarteriosclerotic; gene therapy; cell proliferative disorder;  
KW autoimmune disorder; inflammatory disorder; neurological disorder;  
KW gastrointestinal disorder; cancer; inflammation; atherosclerosis;  
KW epilepsy; diarrhoea.

XX OS Homo sapiens.

XX PN WO200112662-A2.

XX PD 22-FEB-2001.

XX PF 14-AUG-2000; 2000WO-US022315.

XX PR 17-AUG-1999; 99US-0149641P.

XX PR 09-NOV-1999; 99US-0164283P.

XX PA (INCY-) INCYTE GENOMICS INC.

XX PI Lai P, Yue H, Tang YT, Bandman O, Burford N, Azimzai Y;

XX PI Baughn MR, Lu DAM, Patterson C;

XX DR WPI; 2001-168860/17.

XX DR N-ESDB; AAF81768.

XX PT Isolated polypeptide with a human membrane associated protein sequence is

XX PT useful for the diagnosis, prevention and treatment of cell proliferative,

XX PT autoimmune/inflammatory, neurological and gastrointestinal disorders.

XX PS Claim 1; Page 139-140; 173pp; English.

XX CC AAF81741 to AAP81777 encode the human membrane associated proteins

XX CC (MEMAP) given in AAB74695 to AAB74731. MEMAPs have cytostatic,

XX CC antiinflammatory, anticonvulsant, immunosuppressive, antidiarrheic and

XX CC antiarteriosclerotic activities, which can be used in gene therapy.

XX CC MEMAPs and agonist of MEMAPs can be used to treat a disease or condition

XX CC associated with decreased expression of functional MEMAP and antagonists

Abu85826 Human PRO  
Abu98986 Novel hum  
Abu98201 Novel hum  
Abu91907 Novel hum  
Abu99600 Human PRO  
Abu86441 Human sec  
Abu67654 Human sec  
Abu80682 Human PRO  
Abu99600 Human sec  
Abu98990 Human sec  
Abu16513 Human sec  
Abu92413 Human sec  
Abu19054 Human sec  
Abu78475 Human sec  
Abu85211 Novel hum  
Abu00350 Novel hum  
Abu11682 Human sec  
Abu02327 Human sec  
Abu88901 Novel hum  
Abu83596 Human sec

26 2260 99.8 458 6 ABU85826  
27 2260 99.8 458 6 ABU98986  
28 2260 99.8 458 6 ABU98201  
29 2260 99.8 458 6 ABU91907  
30 2260 99.8 458 6 ABU99600  
31 2260 99.8 458 6 ABU86441  
32 2260 99.8 458 6 ABU67654  
33 2260 99.8 458 6 ABU80682  
34 2260 99.8 458 6 ABU99600  
35 2260 99.8 458 6 ABU98990  
36 2260 99.8 458 6 ABU16513  
37 2260 99.8 458 6 ABU92413  
38 2260 99.8 458 6 ABU19054  
39 2260 99.8 458 6 ABU78475  
40 2260 99.8 458 6 ABU85211  
41 2260 99.8 458 6 ABU00350  
42 2260 99.8 458 6 ABU11682  
43 2260 99.8 458 6 ABU02327  
44 2260 99.8 458 6 ABU88901  
45 2260 99.8 458 6 ABU83596

of MEMAP are used to treat a disease or condition associated with overexpression of functional MEMAP. These disorders include cell proliferative, autoimmune/inflammatory, neurological and gastrointestinal disorders. The MEMAP polynucleotides and proteins are also used for the diagnosis of these disorders. Specific examples of these disorders include cancer, inflammation, atherosclerosis, epilepsy and diarrhoea. MEMAP proteins can be used to screen for compounds which specifically bind MEMAP including antibodies, oligonucleotides, proteins and small molecules. MEMAP polynucleotides can be used to prepare transgenic animals which can be studied to provide information concerning human disease. Anti-MEMAP antibodies are useful in immunoassays for the detection of MEMAP protein and can be used as antagonists to treat or prevent a disorder associated with MEMAP. Polynucleotides encoding MEMAP can be delivered to target cells with genetic abnormalities with respect to the expression of MEMAP to treat or prevent a disorder associated with MEMAP.

Sequence 458 AA;

Query Match	100.0%;	Score 2265;	DB 4;	Length 458;
Best Local Similarity	100.0%;	Pred. No. 7.7e-228;		
Matches 458;	Conservative	0;	Mismatches 0;	Indels 0;
Gaps 0;				

QY	1	MAWASRLGLLLALLLPVVGASTPGTVVRINKAALSYVSEIGKAPIQORALQVTVPHFLDWS	60
Db	1	MAWASRLGLLLALLLPVVGASTPGTVVRINKAALSYVSEIGKAPIQORALQVTVPHFLDWS	60
QY	61	GEALQPTRIRILNVHVPRLHLKFTIAGFGVRLLAAANFTFKVPRAPPELELTIPVELLADT	120
Db	61	GEALQPTRIRILNVHVPRLHLKFTIAGFGVRLLAAANFTFKVPRAPPELELTIPVELLADT	120
QY	121	RVTQSSRTPTPVWSISACSLFSGCHANEFGCSNSTSHALLVLVQKHIKAVLSNKLCLISINL	180
Db	121	RVTQSSRTPTPVWSISACSLFSGCHANEFGCSNSTSHALLVLVQKHIKAVLSNKLCLISINL	180
QY	181	VOGVNVHLGTLIGLNPVGPESQIRYSVMVSVPTVTSDIYLSLENAVLFLLGKPIIIPDTAT	240
Db	181	VOGVNVHLGTLIGLNPVGPESQIRYSVMVSVPTVTSDIYLSLENAVLFLLGKPIIIPDTAT	240
QY	241	PFVLPVRHVGTEGSMATVGLSQQLFDSALLLQKAGALNLDITQQLRSDDNLIINTSALGRL	300
Db	241	PFVLPVRHVGTEGSMATVGLSQQLFDSALLLQKAGALNLDITQQLRSDDNLIINTSALGRL	300
QY	301	IPEVARQFPEPMPPVVLKVRIGATPVAMLHTNNATLRLQPFVEVLATASNPASQISFLDQ	360
Db	301	IPEVARQFPEPMPPVVLKVRIGATPVAMLHTNNATLRLQPFVEVLATASNPASQISFLDQ	360
QY	361	VVNLRQLQSYSVKVKLOQTTSVLGPDVQLTVASSNNVGFIDTDQVRLTMGTVEFKPLLDHNA	420
Db	361	VVNLRQLQSYSVKVKLOQTTSVLGPDVQLTVASSNNVGFIDTDQVRLTMGTVEFKPLLDHNA	420
QY	421	LLAMGTLPGVNLHYVAPEIFVTEGVVTVSSGLFYQS	456
Db	421	LLAMGTLPGVNLHYVAPEIFVTEGVVTVSSGLFYQS	456

## RESULT 2

ABB08889

ID	ABB08889	standard;	protein;	458 AA.

XX

AC ABBQ

14-00000

14-JUN-2002 (first entry)  
XX

Human BPIL 196-2 SEO ID NO 4

XX

KW Euma

KW ant

KW  
1 mmu

Cell	Cell
1	2
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97	98
99	100

XX  
vac

OS Home

2000

XX PN XX PD PF FX PR PR PR FR XX PA XX PI XX DR DR XX PT PT PT XX PS XX CC CC CC CC CC CC CC CC CC CC CC CC CC CC SQ

Query Match

Best Local Similarity 100.0%; Pred. No. 7.7e-228;

Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QV 1 MAWASRLGLLLALLLPVVGASTPGTVVRLNKAALSYVSEIGKAPLORALQVTVPHETJWS 60

1. ☐ **Mr.**  
 2. ☐ **Mrs.**  
 3. ☐ **Ms.**  
 4. ☐ **Dr.**  
 5. ☐ **Prof.**  
 6. ☐ **Rev.**  
 7. ☐ **Mr.**  
 8. ☐ **Mrs.**  
 9. ☐ **Ms.**  
 10. ☐ **Dr.**  
 11. ☐ **Prof.**  
 12. ☐ **Rev.**  
 13. ☐ **Mr.**  
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 16. ☐ **Dr.**  
 17. ☐ **Prof.**  
 18. ☐ **Rev.**  
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 22. ☐ **Dr.**  
 23. ☐ **Prof.**  
 24. ☐ **Rev.**  
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 143. ☐ **Prof.**  
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 149. ☐ **Prof.**  
 150. ☐ **Rev.**  
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 153. ☐ **Ms.**  
 154. ☐ **Dr.**  
 155. ☐ **Prof.**  
 156. ☐ **Rev.**  
 157. ☐ **Mr.**  
 158. ☐ **Mrs.**  
 159. ☐ **Ms.**  
 160. ☐ **Dr.**  
 161. ☐ **Prof.**  
 162. ☐ **Rev.**  
 163. ☐ **Mr.**  
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 165. ☐ **Ms.**  
 166. ☐ **Dr.**  
 167. ☐ **Prof.**  
 168. ☐ **Rev.**  
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 170. ☐ **Mrs.**  
 171. ☐ **Ms.**  
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 173. ☐ **Prof.**  
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 186. ☐ **Rev.**  
 187. ☐ **Mr.**  
 188. ☐ **Mrs.**  
 189. ☐ **Ms.**  
 190. ☐ **Dr.**  
 191. ☐ **Prof.**

Db 1 MAWASRLGLLLALLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQRALQVTPHFLDWS 60

Q. Now, did you see any of the other people who were in the car with you?

01 GEATQFINRIRIENHVHPKHLNF IAGFGVRLLAATNF I KVFRAPEPDELILPVELLADI 12

Db 61 GEALQPTRIRILNVHVPRHLKFIAGFGVRLLAANETFKVFRAPPELEITLPVELLADT 120

QY  
121 RVIQSSIRTPVWSISACSLFSGCHANEFDGSNSTSHALLVLVQKHIKAVLSNKLCLSISNL 1800

121 RYUOSSITRTPVWVSTASCSFESGHANEFGNSTSHALIVIVOKHIKAYVSNKICISTSNIT. 180

NOT FIRST OCCURRENCE A COPY OF A F4 CERTIFICATE OF QUALIFICATION IN CONNECTION WITH A F4 VENDOR CONTRACT SHALL BE REQUIRED.

Qy 181 VQGVNVHLGTLIGLNPVGPESQIRYSM'SVPTVTSDYISLEVNAVLFLLGKPIILPTDAT 24C

[illegible]

DB 181 VQGVNVHLGTLIGLNFVGPESQIRYSMVSVPTVTSDIISLEVNVLFLGKPIILPTDAT 240

241 PFVLPRHVGTEGSMATVGLSOOLFDSALLLLLOKAGAI.NL.DITGCLRSDDNLI.NTSAIGRI. 300

QY 421 LLAMGIALPGVNNLHYVAPEIFVYEGYVVISGLFYQS 458  
 DB 421 LLAMGIALPGVNNLHYVAPEIFVYEGYVVISGLFYQS 458

RESULT 3  
 AAU14479  
 ID AAU14479 standard; protein; 458 AA.  
 XX  
 AC AAU14479;  
 XX  
 DT 24-OCT-2001 (first entry)  
 XX  
 DE Human novel protein #350.  
 XX  
 KW Human; novel protein; Antianaemic; osteopathic; antiinflammatory;  
 KW immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic;  
 KW anticonvulsant; antiallergic; cerebroprotective; antifungal; antiviral;  
 KW antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;  
 KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;  
 KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;  
 KW tissue regeneration; immune disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200155437-A2.  
 XX  
 PD 02-AUG-2001.  
 XX  
 XX 25-JAN-2001; 2001WO-US002623.  
 XX  
 PR 25-JAN-2000; 2000US-00491404.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Liu C, Drmanac RT;  
 XX  
 DR WPI; 2001-451939/48.  
 DR N-PSDB; AAS22784.  
 XX

Isolated polypeptides useful for treating anti-inflammatory diseases,  
 nervous system disorders, and for regenerating bone and cartilage.

Example 4; Page 836-837; 894pp; English.

The invention relates to polynucleotides encoding novel human proteins or  
 their active domains. The polypeptides, polynucleotides and antibodies  
 raised against the polypeptides are used in a method of treatment of a  
 mammal and prevention of disorders caused by the aberrant protein  
 expression or activity. The polypeptides can be used as molecular weight  
 markers, food supplements, and in antibody production. The polypeptides  
 are used to identify compounds which bind to the polypeptides.  
 Polynucleotides of the invention are used as probes and primers, for  
 sequencing, for chromosome or gene mapping, in the production of  
 recombinant proteins, and in generating anti-sense DNA or RNA and in gene  
 therapy. Polypeptides of the invention can be used to target drugs to a  
 tumour, in assays to determine biological activity, to raise  
 antibodies/ elicit an immune response, to determine quantitative protein  
 levels, as tissue markers, and to isolate receptors or ligands.  
 Polypeptides of the invention may also be useful in treating platelet  
 disorders, stem cell disorders, regenerating bone, cartilage, tendon,  
 ligament and/or nerve tissue, wound healing, treating burns, promoting  
 the proliferation, differentiation and survival of stem cells, as a  
 contraceptive, treating osteoporosis and osteoarthritis, anaemia,  
 Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral  
 sclerosis, stroke, immune deficiencies resulting from bacterial, viral or  
 fungal infection or from autoimmunity, cancer, allergy, asthma, graft-  
 versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory  
 diseases, nervous system disorders, and infection. The present sequence  
 represents a protein of the invention

Sequence 458 AA;

Query Match 100.0%; Score 2265; DB 4; Length 458;  
 Best Local Similarity 100.0%; Pred. No. 7, 7e-228;  
 Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAWASRLGLLLALLPVGASTPGTVVRLNKAALSYVSEIGKAPLQALQVTVPHFLDWS 60  
 DB 1 MAWASRLGLLLALLPVGASTPGTVVRLNKAALSYVSEIGKAPLQALQVTVPHFLDWS 60  
 QY 61 GEALQPTRIRILNVHVRHLKFIAGFGVRLAAANFTEKVPRAPELETLFVELLADT 120  
 DB 61 GEALQPTRIRILNVHVRHLKFIAGFGVRLAAANFTEKVPRAPELETLFVELLADT 120  
 QY 121 RVTQSSIRTPVVSISACSLFSGHANEFDGNSNSTSEALLVLVQKHIAVLSNKLCLISNLS 180  
 DB 121 RVTQSSIRTPVVSISACSLFSGHANEFDGNSNSTSEALLVLVQKHIAVLSNKLCLISNLS 180  
 QY 181 VQGVNVHLGTLGLNVPVPESQIRYSMVSVPTVSDYISLEVNAMLFLGKFIILPTDAT 240  
 DB 181 VQGVNVHLGTLGLNVPVPESQIRYSMVSVPTVSDYISLEVNAMLFLGKFIILPTDAT 240  
 QY 241 PFVLPVRHVTGEGSMATVGLSQQLFDSALLLLQKAGALNLDITGQLRSDDNLTNSALGRL 300  
 DB 241 PFVLPVRHVTGEGSMATVGLSQQLFDSALLLLQKAGALNLDITGQLRSDDNLTNSALGRL 300  
 QY 301 IPEVARQPEPMPVVLKVLGATPVAMLHTNNATLRLQPFVEVLATASNSAFCSLFLSDV 360  
 DB 301 IPEVARQPEPMPVVLKVLGATPVAMLHTNNATLRLQPFVEVLATASNSAFCSLFLSDV 360  
 QY 361 VVNLRLQLSVSKVLOGTTSLVGDVOLTVAASNVGFIIDTQVRLTGMGTVEKPLDHLNA 420  
 DB 361 VVNLRLQLSVSKVLOGTTSLVGDVOLTVAASNVGFIIDTQVRLTGMGTVEKPLDHLNA 420  
 QY 421 LLAMGIALPGVNNLHYVAPEIFVYEGYVVISGLFYQS 458  
 DB 421 LLAMGIALPGVNNLHYVAPEIFVYEGYVVISGLFYQS 458

## RESULT 4

AAU14243  
 ID AAU14243 standard; protein; 458 AA.  
 XX  
 AC AAU14243;  
 XX  
 DT 24-OCT-2001 (first entry)  
 XX  
 DE Human novel protein #114.  
 XX

KW Human; novel protein; Antianaemic; osteopathic; antiinflammatory;  
 KW immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic;  
 KW anticonvulsant; antiallergic; cerebroprotective; antifungal; antiviral;  
 KW antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;  
 KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;  
 KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;  
 KW tissue regeneration; immune disorder.

OS Homo sapiens.

XX WO200155437-A2.  
 XX

XX 02-AUG-2001.  
 XX

XX 25-JAN-2001; 2001WO-US002623.  
 XX

XX 25-JAN-2000; 2000US-00491404.  
 XX

XX (HYSE-) HYSEQ INC.  
 XX

XX Tang YT, Liu C, Drmanac RT;  
 XX

XX WPI; 2001-451939/48.  
 XX

XX N-PSDB; AAS22548.  
 XX

PT Isolated polypeptides useful for treating anti-inflammatory diseases,



PT nervous system disorders, and for regenerating bone and cartilage.

PS Example 4; Page 590-591; 894pp; English.

XX The invention relates to polynucleotides encoding novel human proteins or  
XX their active domains. The polypeptides, polynucleotides and antibodies  
CC raised against the polypeptides are used in a method of treatment of a  
CC mammal and prevention of disorders caused by the aberrant protein  
CC expression or activity. The polypeptides can be used as molecular weight  
CC markers, food supplements, and in antibody production. The polypeptides  
CC are used to identify compounds which bind to the polypeptides  
CC polynucleotides of the invention are used as probes and primers, for  
CC sequencing, for chromosome or gene mapping, in the production of  
CC recombinant proteins, and in generating anti-sense DNA or RNA and in gene  
CC therapy. Polypeptides of the invention can be used to target drugs to a  
CC tumour, in assays to determine biological activity, to raise  
CC antibodies/elicit an immune response, to determine quantitative protein  
CC levels, as tissue markers, and to isolate receptors or ligands.  
CC Polypeptides of the invention may also be useful in treating platelet  
CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,  
CC ligament and/or nerve tissue, wound healing, treating burns, promoting  
CC the proliferation, differentiation and survival of stem cells, as a  
CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,  
CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral  
CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or  
CC fungal infection or from autoimmunity, cancer, allergy, asthma, graft-  
CC versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory  
CC diseases, nervous system disorders, and infection. The present sequence  
XX represents a protein of the invention

SQ Sequence 458 AA;

Query Match 100.0%; Score 2265; DB 4; Length 458;  
Best Local Similarity 100.0%; Pred. No. 7.7e-228;  
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAWASRLGLLALLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQALQVTVPHFLDWS 60  
Db 1 MAWASRLGLLALLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQALQVTVPHFLDWS 60  
Qy 61 GEALQPTIRILNVHVPRLHLKFIAGFGVRLIAAANFTKVPRAPELELTLPVELLADT 120  
Db 61 GEALQPTIRILNVHVPRLHLKFIAGFGVRLIAAANFTKVPRAPELELTLPVELLADT 120  
Qy 121 RVTQSSIRTPVWSISACSLFSGHANFPGSNTSHALLVLVQKHIAVLSNKLCLISNLL 180  
Db 121 RVTQSSIRTPVWSISACSLFSGHANFPGSNTSHALLVLVQKHIAVLSNKLCLISNLL 180  
Qy 181 VQGVNVHLGTILGLNPVGPSCIRYSMVSVPTVTSYLSLEVNVLFLGKPIILPTDAT 240  
Db 181 VQGVNVHLGTILGLNPVGPSCIRYSMVSVPTVTSYLSLEVNVLFLGKPIILPTDAT 240  
Qy 241 FVILPRHVGTEGSMATVGLSQQLFDSALLLQKAGALNLDITGQLRSDNLLNTSALGRL 300  
Db 241 FVILPRHVGTEGSMATVGLSQQLFDSALLLQKAGALNLDITGQLRSDNLLNTSALGRL 300  
Qy 301 IPEVARQFEHPMPVVLKRLGATPVAMLTNATLRLQFFVEVLATASNSAFQSLFSLDV 360  
Db 301 IPEVARQFEHPMPVVLKRLGATPVAMLTNATLRLQFFVEVLATASNSAFQSLFSLDV 360  
Qy 361 VVNLRLQLSVSKVQLQGTTSVLGVDQVLTAVSSNVGFIPTDQVRLMGTVFEKELLHLNA 420  
Db 361 VVNLRLQLSVSKVQLQGTTSVLGVDQVLTAVSSNVGFIPTDQVRLMGTVFEKELLHLNA 420  
Qy 421 LLANGIALPGVNLHYVAPEIFVYEGYVWISSGLFYQS 458  
Db 421 LLANGIALPGVNLHYVAPEIFVYEGYVWISSGLFYQS 458

RESULT 5

AAU09947

ID AAU09947 standard; protein; 458 AA.

XX

AC

XX

DT 18-JUN-2002 (first entry)

XX

DE Human (new lipid binding protein 1) NLIBP1.

XX

KW Human; new lipid binding protein 1; NLIBP1; cytostatic; antibacterial;  
KW immunosuppressive; tranquilliser; vulnery; haemostatic; cancer; tumour;  
KW bacteraemia; endotoxaemia; meningococcal disease; haemorrhagic trauma;  
KW partial hepatectomy; peritoneal infection; cystic fibrosis.

XX

OS Homo sapiens.

XX

PN WO200177148-A2.

XX

PD 18-OCT-2001.

XX

PF 04-APR-2001; 2001WO-EP003794.

XX

PR 05-APR-2000; 2000EP-00107354.

XX

PA (MERE ) MERCK PATENT GMBH.

XX

PI Grell M, Duecker K, Hoheisel J, Frohme M;

XX

WPI; 2002-010891/01.

DR

N-PSDB; AAS15769.

XX

PT New lipid binding protein 1 polypeptides and polynucleotides useful for  
PT diagnosis and treatment of cancer, bacteraemia, endotoxaemia, peritoneal  
PT infections, cystic fibrosis and identifying modulators of therapeutic  
PT use.

Claim 2; Page 36; 36pp; English.

XX

CC The present invention relates to a new isolated lipid binding protein 1  
CC (NLIBP1) polypeptide chosen from a 458 residue amino acid sequence, fully  
CC defined in the specification, a polypeptide comprising or having 95 %  
CC identity to the 458 residue amino acid, fragments or variants of NLIBP1  
CC and a polypeptide encoded by a 1812 base pair sequence, also fully  
CC defined in the specification. NLIBP1 polypeptide is useful in screening  
CC assays to identify compounds that stimulate or inhibit the function or  
CC level of the polypeptide. NLIBP1 polypeptides, polynucleotides and their  
CC agonists and antagonists are useful for treating cancer, bacteraemia,  
CC endotoxaemia, meningococcal disease, haemorrhagic trauma, partial  
CC hepatectomy, severe peritoneal infections and cystic fibrosis. The NLIBP1  
CC polypeptides and polynucleotides are also useful as vaccines. NLIBP1  
CC polypeptides are useful for identifying membrane bound or soluble  
CC receptors. The molecules of the invention are useful for the recombinant  
CC production of NLIBP1 polypeptides, in diagnostic assays by detecting  
CC mutations in the associated gene, for chromosome localisation studies,  
CC tissue expression studies and for producing transgenic animals useful in  
CC drug discovery and target validation. The present sequence represents the  
CC new lipid binding protein 1 (NLIBP1) that was used in the methods of the  
CC invention

SQ Sequence 458 AA;

Query Match 100.0%; Score 2265; DB 5; Length 458;

Best Local Similarity 100.0%; Pred. No. 7.7e-228;

Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAWASRLGLLALLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQALQVTVPHFLDWS 60

Db 1 MAWASRLGLLALLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQALQVTVPHFLDWS 60

Qy 61 GEALQPTIRILNVHVPRLHLKFIAGFGVRLIAAANFTKVPRAPELELTLPVELLADT 120

Db 61 GEALQPTIRILNVHVPRLHLKFIAGFGVRLIAAANFTKVPRAPELELTLPVELLADT 120

Qy 121 RVTQSSIRTPVWSISACSLFSGHANFPGSNTSHALLVLVQKHIAVLSNKLCLISNLL 180

Db 121 RVTQSSIRTPVWSISACSLFSGHANFPGSNTSHALLVLVQKHIAVLSNKLCLISNLL 180



QY 181 VQGVNHLGTLGLNPVGPESQIRYSMVSVPTVTSYISLEVNVLFLGKPIILPTDAT 240  
 Db 181 VQGVNHLGTLGLNPVGPESQIRYSMVSVPTVTSYISLEVNVLFLGKPIILPTDAT 240  
 QY 241 PFVLPVRHVGTSGMATVGLSQQLFDSALLLQKAGALNLDITGQRLSDNLLNTSALGRL 300  
 Db 241 PFVLPVRHVGTSGMATVGLSQQLFDSALLLQKAGALNLDITGQRLSDNLLNTSALGRL 300  
 QY 301 IPEVARQPEPMPVVLKVRIGATPVAMLHTNNATLRLOPFVEVLATASNSAFQSLFSLDV 360  
 Db 301 IPEVARQPEPMPVVLKVRIGATPVAMLHTNNATLRLOPFVEVLATASNSAFQSLFSLDV 360  
 QY 361 VVNLRLQLSVSKVKLGTTSLVGLDQVLTAVASSNVGFIIDTQVRLTGMGTVEKPLDLHLNA 420  
 Db 361 VVNLRLQLSVSKVKLGTTSLVGLDQVLTAVASSNVGFIIDTQVRLTGMGTVEKPLDLHLNA 420  
 QY 421 LLAMGIALPGVNVNHLHYVAPEIFVYEGYVVISGLFYQS 458  
 Db 421 LLAMGIALPGVNVNHLHYVAPEIFVYEGYVVISGLFYQS 458

RESULT 6  
 ADE85847  
 ID ADE85847 standard; protein; 458 AA.

XX ADE85847;

DT 29-JAN-2004 (first entry)

XX Human antibacterial polypeptide LPLUNC2.

XX Human; antibacterial; LPLUNC2; PLUNC.

XX Homo sapiens.

XX WO2003087143-A2.

XX 23-OCT-2003.

EF 11-APR-2003; 2003WO-GB001583.

XX 12-APR-2002; 2002GB-00008925.

XX (UYSH-) UNIV SHEFFIELD.

XX Bingle C, Craven J;

XX WPI; 2003-833705/77.

XX New polypeptides encoded by nucleic acids that map to human chromosome 20q11, useful for treating bacterial infections, e.g. septicemia, tuberculosis, bacteria-associated food poisoning, blood infections, peritonitis.

XX Disclosure; Fig 2; 40pp; English.

XX The present sequence is the protein sequence of human antibacterial polypeptide LPLUNC2. The invention describes a family of 9 human proteins ADE85846-ADE85857 designated as PLUNCs (palate lung and nasal epithelium core) that are encoded by adjacent genes in an approximately 300 kb region on chromosome 20q11. Members of the PLUNC family fall into 2 groups based on their size. Short PLUNCs (SPLUNCs) comprise SPLUNC1, SPLUNC2, SPLUNC3 and SPLUNC7, while long PLUNCs (LPLUNCs) comprise LPLUNC1, LPLUNC2, LPLUNC3, LPLUNC4 and LPLUNC6. The polypeptides can be used to treat bacterial infections, in particular respiratory infections. The infection is caused by *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Enterococcus faecalis*, *Mycobacterium tuberculosis*, *Streptococcus group B*, *Streptococcus pneumoniae*, *Helicobacter pylori*, *Neisseria gonorrhoea*, *Streptococcus group A*, *Borrelia burgdorferi*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Neisseria meningitidis* type B, *Shigella flexneri*, *Escherichia coli*, *Haemophilus influenzae*, *Mycoplasma pneumoniae*, *Pseudomonas aeruginosa*, *Legionella spp.*, *Moraxella*

CC catarrhalis, *Klebsiella pneumoniae*, *Fusobacterium nucleatum* or *Porphyromonas gingivalis*, and is septicemia, tuberculosis, bacteria-associated food poisoning, blood infection, peritonitis, endocarditis, sepsis, meningitis, pneumonia, stomach ulcer, gonorrhoea, step throat, streptococcal-associated toxic shock, necrotizing fascitis, impetigo, histoplasmosis, Lyme disease, gastro-enteritis, dysentery, shigellosis, or periodontal disease (all claimed).

XX Sequence 458 AA;

Query Match 100.0%; Score 2265; DB 7; Length 458;

Best Local Similarity 100.0%; Pred. No. 7.e-228; Indels 0; Gaps 0;

Matches 458; Conservative 0; Mismatches 0;

QY 1 MAWASRLGLLALLPVVGASTPGTVRLNKAALSYVSEIGKAPLQALQVTPHFLDWS 60

Db 1 MAWASRLGLLALLPVVGASTPGTVRLNKAALSYVSEIGKAPLQALQVTPHFLDWS 60

QY 61 GEALQPTRIRILNVHVRHLKFIAGFGRVLLAAANFTFKVFRAPPELTLPEVLLADT 120

Db 61 GEALQPTRIRILNVHVRHLKFIAGFGRVLLAAANFTFKVFRAPPELTLPEVLLADT 120

QY 121 RVTQSSIRTEPVVISACSLFSGHANEFDGNSGTSHALLVVKHKAIVLSNKLCLISNL 180

Db 121 RVTQSSIRTEPVVISACSLFSGHANEFDGNSGTSHALLVVKHKAIVLSNKLCLISNL 180

QY 181 VQGVNHLGTLGLNPVGPESQIRYSMVSVPTVTSYISLEVNVLFLGKPIILPTDAT 240

Db 181 VQGVNHLGTLGLNPVGPESQIRYSMVSVPTVTSYISLEVNVLFLGKPIILPTDAT 240

QY 241 PFVLPVRHVGTSGMATVGLSQQLFDSALLLQKAGALNLDITGQRLSDNLLNTSALGRL 300

Db 241 PFVLPVRHVGTSGMATVGLSQQLFDSALLLQKAGALNLDITGQRLSDNLLNTSALGRL 300

QY 301 IPEVARQPEPMPVVLKVRIGATPVAMLHTNNATLRLOPFVEVLATASNSAFQSLFSLDV 360

Db 301 IPEVARQPEPMPVVLKVRIGATPVAMLHTNNATLRLOPFVEVLATASNSAFQSLFSLDV 360

QY 361 VVNLRLQLSVSKVKLGTTSLVGLDQVLTAVASSNVGFIIDTQVRLTGMGTVEKPLDLHLNA 420

Db 361 VVNLRLQLSVSKVKLGTTSLVGLDQVLTAVASSNVGFIIDTQVRLTGMGTVEKPLDLHLNA 420

QY 421 LLAMGIALPGVNVNHLHYVAPEIFVYEGYVVISGLFYQS 458

Db 421 LLAMGIALPGVNVNHLHYVAPEIFVYEGYVVISGLFYQS 458

RESULT 7

AAU29272

ID AAU29272 standard; protein; 458 AA.

XX AAU29272;

XX 18-DEC-2001 (first entry)

XX Human PRO polypeptide sequence #249.

XX PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha; blood; chondrocyte cell; cell proliferation; cell differentiation; colon; adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.

XX Homo sapiens.

XX WO200168848-A2.

XX 20-SEP-2001.

XX 28-FEB-2001; 2001WO-US006520.

XX 01-MAR-2000; 2000WO-US005601.

XX 02-MAR-2000; 2000WO-US005841.

XX 03-MAR-2000; 2000US-0187202P.

PR 06-MAR-2000; 2000US-0186368P.  
 PR 14-MAR-2000; 2000US-0189320P.  
 PR 14-MAR-2000; 2000US-0189328P.  
 PR 15-MAR-2000; 2000WO-US00688A.  
 PR 21-MAR-2000; 2000US-0180828P.  
 PR 21-MAR-2000; 2000US-0191007P.  
 PR 21-MAR-2000; 2000US-0191048P.  
 PR 21-MAR-2000; 2000US-0191314P.  
 PR 28-MAR-2000; 2000US-0192655P.  
 PR 29-MAR-2000; 2000US-0193032P.  
 PR 29-MAR-2000; 2000US-0193053P.  
 PR 30-MAR-2000; 2000WO-US00843P.  
 PR 04-APR-2000; 2000US-0194449P.  
 PR 04-APR-2000; 2000US-0194647P.  
 PR 11-APR-2000; 2000US-0195975P.  
 PR 11-APR-2000; 2000US-0196000P.  
 PR 11-APR-2000; 2000US-0196187P.  
 PR 11-APR-2000; 2000US-0196690P.  
 PR 11-APR-2000; 2000US-0196820P.  
 PR 18-APR-2000; 2000US-0198121P.  
 PR 18-APR-2000; 2000US-0198585P.  
 PR 25-APR-2000; 2000US-0199397P.  
 PR 25-APR-2000; 2000US-0199550P.  
 PR 25-APR-2000; 2000US-0199654P.  
 PR 03-MAY-2000; 2000US-0201516P.  
 PR 17-MAY-2000; 2000WO-US013705.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 30-MAY-2000; 2000WO-US014941.  
 PR 02-JUN-2000; 2000WO-US015264.  
 PR 05-JUN-2000; 2000US-0209832P.  
 PR 28-JUL-2000; 2000WO-US020710.  
 PR 22-AUG-2000; 2000US-00644848.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 08-NOV-2000; 2000WO-US030952.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 20-DEC-2000; 2000WO-US034956.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;  
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;  
 XX  
 DR WPI; 2001-602746/68.  
 DR N-PSDB; AAS46173.  
 XX  
 PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the  
 PT presence of tumors, such as prostate and breast tumors, in mammals and to  
 PT screen for modulators of the compounds.  
 XX  
 PS Claim 11; Fig 498; 774pp; English.  
 XX  
 CC Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.  
 CC The PRO polypeptides and their associated nucleic acids can be used to  
 CC detect the presence of a tumour in a mammal by comparing the level of  
 CC expression of a PRO polypeptide in a test sample of cells from the animal  
 CC and a control sample of normal cells, whereby a higher level of  
 CC expression in the test sample indicates the presence of a tumour in the  
 CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats  
 CC and rabbits but are preferably human. The polypeptides can be used to  
 CC stimulate tumour necrosis factor (TNF) alpha release from human blood,  
 CC when contacted with it. A specific polypeptide can be used to stimulate  
 CC the proliferation or differentiation of chondrocyte cells. The PRO  
 CC proteins can be used to determine the presence of tumours and also  
 CC susceptibility to tumour development, particularly adrenal, lung, colon,  
 CC breast, prostate, rectal, cervical, or liver tumours, in mammalian  
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids  
 CC can be used for genetic analysis of individuals with genetic disorders  
 XX  
 SQ Sequence 458 AA;

Query Match 99.8%; Score 2260; DB 4; Length 458;  
 Best Local Similarity 99.8%; Pred. No. 2.6e-227;  
 Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAWASRLGLLALLLPVVGASTPGTVRLNKAAALSYVSEIGKAPLQALQVTPVPHLWS 60  
 DB 1 MAWASRLGLLALLLPVVGASTPGTVRLNKAAALSYVSEIGKAPLQALQVTPVPHLWS 60  
 QY 61 GEALQPTIRILNVHVPRIHLKFIAGFGVRLIAAANFTFKVPRAPLELTLPVELLADT 120  
 DB 61 GEALQPTIRILNVHVPRIHLKFIAGFGVRLIAAANFTFKVPRAPLELTLPVELLADT 120  
 QY 121 RVTOSSIRTPVVSISACSLFSGHANEPDGSNSTSHALLVLVQKHKAVLSNKLCLISNL 180  
 DB 121 RVTOSSIRTPVVSISACSLFSGHANEPDGSNSTSHALLVLVQKHKAVLSNKLCLISNL 180  
 QY 181 VQGVNVHLGLTILGLNPNVGPESQIRYSMTVSPTVTSYISLEVNNAVLELIGKPIILPTDAT 240  
 DB 181 VQGVNVHLGLTILGLNPNVGPESQIRYSMTVSPTVTSYISLEVNNAVLELIGKPIILPTDAT 240  
 QY 241 PFVLPFRHVGTGSMATVGLSQOLPDSALLLQKAGALNDITGQSRSDNLTNTSALGSL 300  
 DB 241 PFVLPFRHVGTGSMATVGLSQOLPDSALLLQKAGALNDITGQSRSDNLTNTSALGSL 300  
 QY 301 IPEVARQPEPMPVVLKVLGATPVAMLHTNATLRLQPFVEVLATASNAFQSLFSLDV 360  
 DB 301 IPEVARQPEPMPVVLKVLGATPVAMLHTNATLRLQPFVEVLATASNAFQSLFSLDV 360  
 QY 361 VVNLRLQLSVSKVKLQGTTSVLGQVLTVAASNVGFIQDQVRLTLMGTVEKPLLDHLNA 420  
 DB 361 VVNLRLQLSVSKVKLQGTTSVLGQVLTVAASNVGFIQDQVRLTLMGTVEKPLLDHLNA 420  
 QY 421 LLAMGIALPGVNLHYVAPEIFVVEGYVVISGLFYQS 458  
 DB 421 LLAMGIALPGVNLHYVAPEIFVVEGYVVISGLFYQS 458

## RESULT 8

ABE08888  
 ID ABE08888 standard; protein; 458 AA.

XX ABE08888;

XX 14-JUN-2002 (first entry)

XX Human BPIL 196-1 SEQ ID NO 2.

XX Human; bactericidal/permeability increasing factor-like; BPII;  
 XX antimicrobial; bactericidal; cytostatic; antileukaemia; antiinflammatory;  
 XX immunomodulatory; infection; cancer; chemotactic; chemokinetic; cytokine;  
 XX cell proliferation; differentiation; immune response; gene therapy;  
 XX vaccine; protein coordinate data.

XX Homo sapiens.

XX WO200136478-A2.

XX 25-MAY-2001.

XX 20-NOV-2000; 2000WO-US031878.

XX 19-NOV-1999; 99US-00443370.

XX 18-JAN-2000; 2000US-00484597.

XX 22-FEB-2000; 2000US-0183922P.

XX 29-MAR-2000; 2000US-0193400P.

XX (HYSE-) HYSEQ INC.

XX Ballinger DG, Mulero JJ, Qian X, Mize NK, Haley DA, Boyle BJ;

XX WPI; 2001-381225/40.

XX N-PSDB; ABL55895.

XX Polypeptides with bactericidal/permeability increasing factor-like

PT activity, the nucleic acids that encode them, useful for diagnosing

PT and/or treating e.g. microbial infections and cancers.

XX PS Claim 29; Page 10-12; 807pp; English.

XX CC The invention relates to polypeptides (ABB08488-ABB08499) with

XX CC bactericidal/permeability increasing factor-like (BPI/L) activity, the

XX CC nucleic acids that encode them (ABL55895-ABL55906) and methods and

XX CC apparatus for detecting them and modulating their activity. The proteins

XX CC have antimicrobial, bactericidal, cytostatic, antileukemia,

XX CC antiinflammatory and immunomodulatory activity. The nucleic acids,

XX CC polypeptides and methods may be used for detecting and treating

XX CC pathologies associated with expression of BPI/L polypeptides, e.g. for the

XX CC treatment and diagnosis of microbial infections (especially by Gram

XX CC negative bacteria), cancers (especially leukaemia), inflammation,

XX CC disorders of chemotactic/chemokinetic activity and disorders of cytokine

XX CC and cell proliferation/differentiation activity, to stimulate/suppress

XX CC immune responses

XX SQ Sequence 458 AA;

Query Match 99.8%; Score 2260; DB 4; Length 458;

Best Local Similarity 99.8%; Pred. No. 2.6e-227;

Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAWASRLGLALLPVVVGASTPGTWRINKAALSVVSEIGKAPLQALQVTPHFLDWS 50

DB 1 MAWASRLGLALLPVVVGASTPGTWRINKAALSVVSEIGKAPLQALQVTPHFLDWS 60

QY 61 GEALQPTIRILNVHVPRLHLKFIAGFGVRLAAANFTPKVRAPEPLELTLPVELLADT 120

DB 61 GEALQPTIRILNVHVPRLHLKFIAGFGVRLAAANFTPKVRAPEPLELTLPVELLADT 120

QY 121 RVTQSSIRTPVVISACSLFSGHANFEDGNSNSTSHALLVVKHKAVLSNKLCLSTSLN 180

DB 121 RVTQSSIRTPVVISACSLFSGHANFEDGNSNSTSHALLVVKHKAVLSNKLCLSTSLN 180

QY 131 VQGVNVHGLTILGNVPESQIRVSMVSVPTSDYISLEVNVLFLGKPIILPTDAT 240

DB 131 VQGVNVHGLTILGNVPESQIRVSMVSVPTSDYISLEVNVLFLGKPIILPTDAT 240

QY 241 PFVLPVRHVTGEGSMATVGLSQFLPSALLLQKAGALNLDITGQLRSDNLLNTSALGRL 300

DB 241 PFVLPVRHVTGEGSMATVGLSQFLPSALLLQKAGALNLDITGQLRSDNLLNTSALGRL 300

QY 301 IPEVARQPEPMPVVLKVLGATPVAMLTNNATLRLQPFVEVLATANSAPQSIFSLDV 360

DB 301 IPEVARQPEPMPVVLKVLGATPVAMLTNNATLRLQPFVEVLATANSAPQSIFSLDV 360

QY 361 VVNLRLQLSVSKVLGGTTSVLGDVQLTVASSNVGFIIDQVRLTNGTVEKPLDLHLNA 420

DB 361 VVNLRLQLSVSKVLGGTTSVLGDVQLTVASSNVGFIIDQVRLTNGTVEKPLDLHLNA 420

QY 421 LLAMGIALPGVNVNLHYVAPEIFVVEGYVVISGLFYQS 458

DB 421 LLAMGIALPGVNVNLHYVAPEIFVVEGYVVISGLFYQS 458

RESULT 9

ABB84977

ID ABB84977 standard; protein; 458 AA.

XX AC ABB84977;

XX DT 16-MAY-2002 (first entry)

XX DE Human PRO5776 protein sequence SEQ ID NO:322.

XX KW Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;

XX KW vulnery; arteriosclerotic; PRO agonist; PRO antagonist; trauma;

XX KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;

XX KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;

XX KW age-related macular degeneration; arterial restenosis; angina;

XX KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;

XX KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;

KW wound healing; chromosome mapping; gene mapping.

XX OS Homo sapiens.

XX WO200200690-A2.

XX 03-JAN-2002.

XX 20-JUN-2001; 2001WO-US019692.

XX 23-JUN-2000; 2000US-0213637P.

XX 20-JUL-2000; 2000US-0219556P.

XX 25-JUL-2000; 2000US-0220624P.

XX 25-JUL-2000; 2000US-0220664P.

XX 28-JUL-2000; 2000WO-US023710.

XX 02-AUG-2000; 2000US-0222695P.

XX 17-AUG-2000; 2000US-00643657.

XX 23-AUG-2000; 2000WO-US023522.

XX 24-AUG-2000; 2000WO-US023328.

XX 07-SEP-2000; 2000US-0236978P.

XX 18-SEP-2000; 2000US-00664610.

XX 18-SEP-2000; 2000US-00665350.

XX 24-OCT-2000; 2000US-0242922P.

XX 08-NOV-2000; 2000US-00709238.

XX 08-NOV-2000; 2000WO-US030952.

XX 10-NOV-2000; 2000WO-US030873.

XX 01-DEC-2000; 2000WO-US032678.

XX 20-DEC-2000; 2000US-00747259.

XX 20-DEC-2000; 2000WO-US034956.

XX 22-JAN-2001; 2001US-00767609.

XX 28-FEB-2001; 2001US-00796498.

XX 28-FEB-2001; 2001WO-US006520.

XX 01-MAR-2001; 2001WO-US006666.

XX 09-MAR-2001; 2001US-00802706.

XX 14-MAR-2001; 2001US-00808689.

XX 22-MAR-2001; 2001US-00816744.

XX 05-APR-2001; 2001US-00828366.

XX 10-MAY-2001; 2001US-00854208.

XX 10-MAY-2001; 2001US-00854280.

XX 25-MAY-2001; 2001US-00866028.

XX 25-MAY-2001; 2001US-00866034.

XX 25-MAY-2001; 2001WO-US017092.

XX 30-MAY-2001; 2001US-00870574.

XX 30-MAY-2001; 2001WO-US017443.

XX 01-JUN-2001; 2001WO-US017800.

XX (GETH ) GENENTECH INC.

XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;

XX Godowski P, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;

XX Stephan JF, Watanabe CK, Williams PM, Wood WL, Ye W;

XX WPI: 2002-090516/12.

XX N-PSDB; ABL88232.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,

XX useful in diagnosis and treatment of cardiovascular (e.g. myocardial

XX infarction), endothelial or angiogenic disorders in a mammal.

XX Claim 11; Fig 322; 565pp; English.

XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to

XX ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,

XX antiangiogenic, hypotensive, vulnery and antiarteriosclerotic

XX activities, and can be used in gene therapy. The PRO polynucleotides,

XX proteins, agonists and antagonists are useful for treating or diagnosing

XX a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.

XX cardiac hypertrophy, trauma, cancer, age-related macular degeneration,

XX atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,

XX angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour

XX angiogenesis (such as breast carcinoma and liver carcinoma) and wound

XX healing. The PRO polynucleotides have applications in molecular biology,

XX including use as hybridisation probes, and in chromosome and gene

CC mapping, ABL88259 to ABL88267 represent primers and probes used in the  
 CC exonification of the present invention

XX Sequence 458 AA;

Query Match 99.8%; Score 2260; DB 5; Length 458;  
 Best Local Similarity 99.8%; Pred. No. 2.6e-227;  
 Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 DB 1 MAWASRLGILLALLPVVGASTGTGTVRLNKALSYSEIGKAPLQALQVTVPHPLDWS 60  
 QY 61 GEALQPTIRILNVHVRHLHAFIAGFGVRLAAANFTKVPRAPELELTLPVELLADT 120  
 DB 61 GEALQPTIRILNVHVRHLHAFIAGFGVRLAAANFTKVPRAPELELTLPVELLADT 120  
 QY 121 RVTQSSIRTPVVISACSLFSGHANFQGSNSTSHALLVLVQKHIAVLSNKLCLISINL 180  
 DB 121 RVTQSSIRTPVVISACSLFSGHANFQGSNSTSHALLVLVQKHIAVLSNKLCLISINL 180  
 QY 181 VQGVNVHLGTLGLNPVGPESQIRYSWSVPTVTSYISLEVNVLFLAGKPIILPTDAT 240  
 DB 181 VQGVNVHLGTLGLNPVGPESQIRYSWSVPTVTSYISLEVNVLFLAGKPIILPTDAT 240  
 QY 241 PFVLPVRHVTEGSMATVGLSQFLDSALLLQKAGALNLDITGQLRSDNLTLSALGRL 300  
 DB 241 PFVLPVRHVTEGSMATVGLSQFLDSALLLQKAGALNLDITGQLRSDNLTLSALGRL 300  
 QY 301 IPEVARQPEPMPVVKVRLGATPVAMLHTNNATLRLQPFVEVLATASNSAFQSLFSLDV 360  
 DB 301 IPEVARQPEPMPVVKVRLGATPVAMLHTNNATLRLQPFVEVLATASNSAFQSLFSLDV 360  
 QY 361 VVNLRLQLSVSKVKGQTTSVLGDVOLTVAASNVGFDITDQVRLMGTVPEKPLLDHLNA 420  
 DB 361 VVNLRLQLSVSKVKGQTTSVLGDVOLTVAASNVGFDITDQVRLMGTVPEKPLLDHLNA 420  
 QY 421 LLAMGIALPGVNLVHVAPEIFVYEGYVVISGLFYQS 458  
 DB 421 LLAMGIALPGVNLVHVAPEIFVYEGYVVISGLFYQS 458

RESULT 10

ID ABB95583  
 AC ABB95583; standard; protein; 458 AA.

XX ABB95583;

DT 19-JUL-2002 (first entry)

XX Human angiogenesis related protein PRO5776 SEQ ID NO: 322.

XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;  
 KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
 KW cardiant; cytostatic; antiangiogenic; hypotensive; vulnery;

XX anti-arteriosclerotic.

OS Homo sapiens.

XX WO200208284-A2.

XX 31-JAN-2002.

XX 09-JUL-2001; 2001WO-US021735.

XX 20-JUL-2000; 2000US-0219556P.

XX 25-JUL-2000; 2000US-0220624P.

XX 28-JUL-2000; 2000US-0220664P.

XX 28-JUL-2000; 2000WO-US020710.

XX 02-AUG-2000; 2000US-0222695P.

XX 17-AUG-2000; 2000US-00643657.

XX 23-AUG-2000; 2000WO-US023522.

XX 24-AUG-2000; 2000WO-US023328.

PR 07-SEP-2000; 2000US-0230978P.  
 PR 18-SEP-2000; 2000US-00664610.  
 PR 18-SEP-2000; 2000US-00665350.  
 PR 24-OCT-2000; 2000US-0242922P.  
 PR 08-NOV-2000; 2000US-00709238.  
 PR 08-NOV-2000; 2000WO-US030952.  
 PR 10-NOV-2000; 2000WO-US030873.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 20-DEC-2000; 2000US-00747259.  
 PR 20-DEC-2000; 2000WO-US034956.  
 PR 22-JAN-2001; 2001US-00767609.  
 PR 28-FEB-2001; 2001US-00796498.  
 PR 28-FEB-2001; 2001WO-US006520.  
 PR 01-MAR-2001; 2001WO-US006666.  
 PR 09-MAR-2001; 2001US-00802706.  
 PR 14-MAR-2001; 2001US-00808689.  
 PR 22-MAR-2001; 2001US-00816744.  
 PR 05-APR-2001; 2001US-00828366.  
 PR 10-MAY-2001; 2001US-00854208.  
 PR 10-MAY-2001; 2001US-00854280.  
 PR 25-MAY-2001; 2001US-00866028.  
 PR 25-MAY-2001; 2001US-00866034.  
 PR 25-MAY-2001; 2001WO-US017092.  
 PR 30-MAY-2001; 2001US-00870574.  
 PR 30-MAY-2001; 2001WO-US017443.  
 PR 01-JUN-2001; 2001WO-US017800.  
 PR 20-JUN-2001; 2001WO-US019692.

XX (GETH ) GENENTECH INC.

PA (BAKE/) BAKER K P.

PA (FERR/) FERRARA N.

PA (GERB/) GERBER H.

PA (GERR/) GERRITSEN M E.

PA (GODD/) GODDARD A.

PA (GODO/) GODOWSKI P J.

PA (GURN/) GURNEY A L.

PA (HILL/) HILLAN K J.

PA (MARS/) MARSTERS S A.

PA (PANU/) PAN J.

PA (PAON/) PAONI N F.

PA (STEP/) STEPHAN J F.

PA (WATA/) WATANABE C K.

PA (WILL/) WILLIAMS P M.

PA (WOOD/) WOOD W I.

XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;

PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;

PI Stephan JF, Watanabe CK, Williams PM, Wood WL, Ye W;

XX WPI; 2002-171999/22.

DR N-PSDB; ABL95721.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,

PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial

PT infarction), endothelial or angiogenic disorders in a mammal.

XX Claim 11; Fig 322; 567pp; English.

XX The present invention provides the protein and coding sequences of human

CC PRO proteins. These are useful for treating or diagnosing a

CC cardiovascular, endothelial or angiogenic disorder, including cardiac

CC hypertrophy, trauma, cancer, age-related macular degeneration,

CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,

CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour

CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound

CC healing. The present sequence is a PRO protein of the invention

XX Sequence 458 AA;

XX Query Match 99.8%; Score 2260; DB 5; Length 458;

XX Best Local Similarity 99.8%; Pred. No. 2.6e-227;

XX Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MAWASRLGULLALLLPVVGASTPGTVRLNKXALSYVSEIGKAPLQALQVTVPHFLDWS 60
DB |||||
QY 1 MAWASRLGULLALLLPVVGASTPGTVRLNKXALSYVSEIGKAPLQALQVTVPHFLDWS 60
DB |||||
QY 61 GEALOPTRIILNVHVRHLKFIAGFGVLLAARNTFKVFRAPPELELTLPVELLAT 120
DB |||||
QY 61 GEALOPTRIILNVHVRHLKFIAGFGVLLAARNTFKVFRAPPELELTLPVELLAT 120
DB |||||
QY 221 RVTQSSIRTPVVISACSLFSGHANEFDSGNS`SHALLVLVQKHAKAVLSNKLCLISNML 180
DB |||||
QY 181 VQGVNHLGTLGLNPVGPESQIRYSMVSVPTVTSYISLEVNNAVLFLLGKPIILPTDAT 240
DB |||||
QY 181 VQGVNHLGTLGLNPVGPESQIRYSMVSVPTVTSYISLEVNNAVLFLLGKPIILPTDAT 240
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QY 241 PVLPRHVCTEGSMATVGLSQQLFDSALLLQKAGALNLDITGQLRSDNLLNTSALGRL 300
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QY 241 PVLPRHVCTEGSMATVGLSQQLFDSALLLQKAGALNLDITGQLRSDNLLNTSALGRL 300
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QY 361 VVNLRLQLSVSKVKGTLGTTSVLGDVOLTVAASNKGPHIDTQVRLTGMGTVPKPLLDHNA 420
DB |||||
QY 421 LLAMGIALPGVNVHLHVAPEIFVYEGYVVISGLFYQS 458
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DB |||||

RESULT 11
ABU58648
ID ABU58648 standard; protein; 458 AA.
XX AC ABU58648;
XX AC ABU58648;
XX DT 15-APR-2003 (first entry)
XX DE Human PRO polypeptide #249.
XX KW Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
XX KW dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;
XX KW antibody-dependent enzyme mediated prodrug therapy.
XX OS Homo sapiens.
XX PN US2003027272-A1.
XX PD 06-FEB-2003.
XX PF 21-JUN-2002; 2002US-00176492.
XX XX
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
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PR 11-MAR-1998;
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PR 15-SEP-1998; 98US-0100388P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 16-SEP-1998; 98US-0101751P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100683P.
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PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
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PR 30-SEP-1998; 98US-0102487P.
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PR 01-OCT-1998; 98US-0102684P.
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PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103449P.
PR 07-OCT-1998; 98US-00168978.

Query Match 99.8%; Score 2260; DB 6; Length 458;
Best Local Similarity 99.8%; Pred. No. 2.6e-227;
Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAWASRLGLLLALLLPWGASTPTGVRLNKAALSYVSEIGKAPLQALQVTVPHFLDWS 60
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Db 61 GEALQPTRIRILNVHVPRLHKEIAGFGVRLAAANFTFKVFRAPPELETLTPVELLADT 120
QY 121 RVTQSSIRTPVWSISACSLPSGHANFEDGNSNSTHALLVLVQKHKAVLSNKLCLSL 180
Db 121 RVTQSSIRTPVWSISACSLPSGHANFEDGNSNSTHALLVLVQKHKAVLSNKLCLSL 180
QY 181 VQGVNHLGLTGLNVPVGPESQIRYSWVPTVTSYISLEVNALFLICKPIILPTDAT 240
Db 181 VQGVNHLGLTGLNVPVGPESQIRYSWVPTVTSYISLEVNALFLICKPIILPTDAT 240
QY 241 PFVLPVHVGTEGSMATVGLSQQLFDSALLLQKAGALNLDITQOLRSDNLLNTSALGRL 300
Db 241 PFVLPVHVGTEGSMATVGLSQQLFDSALLLQKAGALNLDITQOLRSDNLLNTSALGRL 300
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ID ABU88196 standard; protein; 458 AA.
XX AC ABU88196;
XX DT 07-JUL-2003 (first entry)
XX DE Novel human secreted and transmembrane protein PRO5776.
XX KW Human; secreted and transmembrane protein; PRO; gene therapy;
XX KW tumour necrosis factor-alpha release; TNF-alpha release;
XX KW chondrocyte proliferation; chondrocyte differentiation; tumour;
XX KW adrenal tumour; lung tumour; colon tumour; breast tumour;
XX KW prostate tumour; rectal tumour; cervical tumour; liver tumour.
XX OS Homo sapiens.
XX PN US2003032127-A1.
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 AC ABR66385;  
 XX XX  
 DT 05-AUG-2003 (first entry)  
 DE Human secreted polypeptide PRO5776, SEQ ID NO:498.  
 XX XX

Human; PRO; secreted protein; transmembrane protein;  
 extracellular domain; tumour necrosis factor-alpha; TNF-alpha;  
 chondrocyte; proliferation; differentiation; cartilage disorder;  
 bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;  
 adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;  
 liver; drug screening; transgenic animal; genetic analysis;  
 antiarthritic; vulnery; gene therapy.

OS Homo sapiens.

XX XX

PN US2003027278-A1.

XX XX

PD 06-FEB-2003.

XX XX

PF 21-JUN-2002; 2002US-00176987.

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PR 01-OCT-1998; 98US-0102687P.

Query Match 99.8%; Score 2260; DB 6; Length 458;
Best Local Similarity 99.8%; Pred. No. 2.6e-227;
Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAMASRLGLLLALLPVVGASTPCTVYRLNKAALSYVSEIGKAFQRLAQVTVHFLLDWS 60
DB 1 MAMASRLGLLLALLPVVGASTPCTVYRLNKAALSYVSEIGKAFQRLAQVTVHFLLDWS 60
QY 61 GEALQPTRIRILNVHVPRLHLKFTAGFGVRLAAANFTKVFRAPEPELELTPVELLADT 120
DB 61 GEALQPTRIRILNVHVPRLHLKFTAGFGVRLAAANFTKVFRAPEPELELTPVELLADT 120
QY 121 RVTQSSIRTPVWSISACSLFSGHANEFDSNSTSHALLVLVQKHKAVLSNKLCLISNLL 180
DB 121 RVTQSSIRTPVWSISACSLFSGHANEFDSNSTSHALLVLVQKHKAVLSNKLCLISNLL 180
QY 181 VQGVNHLGTLIGLNPVGPESQIRYSMVSVPTVTSYISLEVNAVLELLGKPIILPTDAT 240
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QY 241 PFVLPRLHWGTEGSMATVGLSQQLFDSALLLQKAGALNLTITQRLSDDNLLNTSALGRL 300
DB 241 PFVLPRLHWGTEGSMATVGLSQQLFDSALLLQKAGALNLTITQRLSDDNLLNTSALGRL 300
QY 301 IPEVARQFPEPEMVLKVLGATPVAMLTNNATLRLQPEVEVLATASNAFQSLFSLDV 360
DB 301 IPEVARQFPEPEMVLKVLGATPVAMLTNNATLRLQPEVEVLATASNAFQSLFSLDV 360
QY 361 VVNLRLQLSVKVKGTLGTSVLGDVQITVASSNVGFDITDQVRLMGTVFEKPLLDHNA 420
DB 361 VVNLRLQLSVKVKGTLGTSVLGDVQITVASSNVGFDITDQVRLMGTVFEKPLLDHNA 420
QY 421 LLAMGIALPGVNLHVVAPEIFVYEGYVVISGLFYS 458
DB 421 LLAMGIALPGVNLHVVAPEIFVYEGYVVISGLFYS 458

RESULT 15
ABR65775
ID ABR65775 standard; protein; 458 AA.
XX AC ABR65775;
XX DT 05-AUG-2003 (first entry)
XX DE Human secreted polypeptide PRO5776, SEQ ID NO:498.
XX KW Human; PRO; secreted protein; transmembrane protein;
XX KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
XX KW chondrocyte; proliferation; differentiation; cartilage disorder;
XX KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
XX KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
XX KW liver; drug screening; transgenic animal; genetic analysis;
XX KW antiarthritic; vulnery; gene therapy.
OS Homo sapiens.
XX US2003036159-A1.
XX PD 20-FEB-2003.
XX PF 02-JUL-2002; 2002US-00188773.
XX PR 18-SEP-1997; 97US-0059263P.
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XX PR 17-OCT-1997; 97US-0062250P.
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Query Match          99.8%; Score 2260; DB 6; Length 458;
Best Local Similarity 99.8%; Pred. No. 2,6e-227;
Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 61 GEALQPTRILNVHVRHLKFIAGVGLLAAANFTKVPAPBPBLTLPVELLADT 120
DB 61 GEALQPTRILNVHVRHLKFIAGVGLLAAANFTKVPAPBPBLTLPVELLADT 120

QY 121 RVTOSSIRTPVWSISACSLFSGHANFDSNSTSHALLVLVQKHKAVLSNKLCLISNL 180
DB 121 RVTOSSIRTPVWSISACSLFSGHANFDSNSTSHALLVLVQKHKAVLSNKLCLISNL 180

QY 181 VQGVNHLGTLGLNPVGPESQIRYSNVSVPTVTSYISLEVNVLFLGKPIILPTDAT 240
DB 181 VQGVNHLGTLGLNPVGPESQIRYSNVSVPTVTSYISLEVNVLFLGKPIILPTDAT 240

QY 241 PFVLPRHVGTGSMATVGLSQQLFDSALLLOKAGALNLDITGLRSDDDLNTSALGRL 300
DB 241 PFVLPRHVGTGSMATVGLSQQLFDSALLLOKAGALNLDITGLRSDDDLNTSALGRL 300

QY 301 IPEVARQFPEPMPVVLKVRIGATPVAMLHTNNATLRLQPFVEVLATASNSAFQSLFSLDV 360
DB 301 IPEVARQFPEPMPVVLKVRIGATPVAMLHTNNATLRLQPFVEVLATASNSAFQSLFSLDV 360

QY 361 VYNRLQLSVSKVYKLGTTSVLGDVOLTVAASNVGFTIDQVRLMSTVFEKPLDLHLNA 420
DB 361 VYNRLQLSVSKVYKLGTTSVLGDVOLTVAASNVGFTIDQVRLMSTVFEKPLDLHLNA 420

QY 421 LLAMGIALPGVNLHVHVAPEIFVYGVVWISSGLFYQS 458
DB 421 LLAMGIALPGVNLHVHVAPEIFVYGVVWISSGLFYQS 458
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Search completed: June 29, 2004, 10:58:54  
Job time : 62 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 29, 2004, 21:30:21 ; Search time 7112 Seconds

(without alignments)

7688.084 Million cell updates/sec

Title: US-10-069-034-65

Perfect score: 1831

Sequence: 1 gcctataaagtagcctctg.....ttgagtcgcaaaaaaaaaa 1831

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: em\_estba:\*\*

2: em\_esthum:\*\*

3: em\_estin:\*\*

4: em\_estmu:\*\*

5: em\_estov:\*\*

6: em\_estro:\*\*

7: em\_estro:\*\*

8: em\_htc:\*\*

9: gb\_est1:\*\*

10: gb\_est2:\*\*

11: gb\_estc:\*\*

12: gb\_est3:\*\*

13: gb\_est4:\*\*

14: gb\_est5:\*\*

15: em\_estfun:\*\*

16: em\_estom:\*\*

17: em\_gss\_fun:\*\*

18: em\_gss\_inv:\*\*

19: em\_gss\_pln:\*\*

20: em\_gss\_vit:\*\*

21: em\_gss\_fun:\*\*

22: em\_gss\_mam:\*\*

23: em\_gss\_mus:\*\*

24: em\_gss\_pro:\*\*

25: em\_gss\_rod:\*\*

26: em\_gss\_phg:\*\*

27: em\_gss\_vrl:\*\*

28: gb\_gss1:\*\*

29: gb\_gss2:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1377	75.2	1377	29	AY417102	AY417102 Homo sapi
2	1314	71.8	1377	29	AY417103	AY417103 Pan trogl
3	875.2	47.8	1703	11	AK009619	AK009619 Mus muscu
4	875.2	47.8	1705	11	AK028158	AK028158 Mus muscu

5	874.6	47.8	1696	11	AK009346
6	870.4	47.5	1699	11	AK075874
7	868.8	47.4	1701	11	AK028156
8	856.2	46.8	1679	11	AK010130
9	854.4	46.7	1693	11	AK010215
10	853.4	46.6	1688	11	AK009776
11	853	46.6	1727	11	AK010157
12	849.2	46.4	1698	11	AK010154
13	848	46.3	1700	11	AK009504
14	815.6	44.5	1389	29	AY417104
15	812.6	44.4	1699	11	AK009871
16	800.6	43.7	1688	11	AK009794
17	769.8	42.0	819	12	BI489783
18	677	37.0	1307	11	AK009754
19	560.4	30.6	578	13	EX487536
20	539	29.4	539	13	EX280449
21	477.8	26.1	1003	13	BY789668
22	466.2	25.5	883	13	BY709288
23	464	25.3	1013	13	BY709115
24	463.2	25.3	480	9	AJ403124
25	454.4	24.8	998	13	BY709211
26	435.6	23.8	453	9	AJ403122
27	423.2	23.4	982	13	BY709415
28	403.4	22.3	427	14	CD697627
29	396.8	21.7	737	10	BB610562
30	388.6	21.2	729	10	BB610508
31	371.6	20.3	712	10	BB610518
32	371.6	20.3	754	10	BB610661
33	296.2	18.2	650	12	BI490756
34	292.8	18.0	757	9	AV090749
35	291.6	15.9	747	9	AV089480
36	284.8	15.6	556	10	BB610620
37	277.4	15.2	543	10	BB610635
38	273.8	15.0	750	9	AV092418
39	239.8	13.1	589	12	BI279481
40	221.8	12.1	225	10	AW155639
41	179.8	9.8	184	9	AI834221
42	130.8	7.1	293	10	BB565312
43	122.4	6.7	146	10	AW444867
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## ALIGNMENTS

RESULT 1  
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LOCUS Homo sapiens HCM6112 gene, VIRTUAL TRANSCRIPT, partial sequence, 1377 bp DNA linear GSS 12-DEC-2003  
DEFINITION Genomic survey sequence.  
ACCESSION AY417102 GI:39773062  
VERSION AY417102.1  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 1377)  
AUTHORS Clark,A.G., Glancowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 1377)  
AUTHORS Clark,A.G., Glancowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.  
TITLE Direct Submission



[illegible]

961	Db	GGTGCACACCTGTGCGCATGCTCCACAAAACAGCCACCGCTGCGCTGCAGGCCCTTC	1020
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1021	Db	GTGGAGGTCCTGGCCACAGCTCCAACTCGCTTTCCAAATCCCTCTCTCCCTGGATGSG	1080
1206	Qy	GTAGTCAACTTGAGACTTCAGAGCTCTCTGTCTCAAGGTGAAGCTTCAGGGGACACGCTCT	1265
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1266	Qy	GTCTCGGGGATGTCCAGGCTCACGGTGGGCTCTCTCCAAAGTGGSCTTCATGTATCAGAT	1325
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1201	Db	CAGGTGCGCACACTGATGGGCACCGTTTTTGAAGAAGCCCTGCTGGACCACTCCATGCT	1260
1386	Qy	CTCTTGGCCATGGGAATGCGCTCCCTGGTGGTGGTCAACCTCCACTATGTGGCCCCCTGAG	1445
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1446	Qy	ATCTTTGTCTATGAGGGCTACGTGGTGATATCCAGTGGACTCTCTCTACCAAGACTGA	1502
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RESULT 3	AK009619	1703 bp	mRNA	linear	HTC 20-SEP-2003
LOCUS	AK009619				
DEFINITION	Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310034f21 product:hypothetical lipid-binding serum glycoprotein containing protein, full insert sequence.				
ACCESSION	AK009619	1	GI:12844522		
VERSION	AK009619.1				
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1	Carninci, P. and Hayashizaki, Y.			
AUTHORS					
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)				
MEDLINE	99279253				
PUBMED	10349636				
REFERENCE	2	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.			
AUTHORS					
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)				
MEDLINE	20499374				
PUBMED	11042159				
REFERENCE	3	Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishii, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Iizawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J., Yoneda, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.			
AUTHORS					
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer				
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)				
MEDLINE	20530913				
PUBMED	11076861				
REFERENCE	4	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.			
AUTHORS					
TITLE	Functional annotation of a full-length mouse cDNA collection				
JOURNAL	Nature 409, 685-690 (2001)				



## REFERENCE AUTHORS

5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
5 (bases 1 to 1703)



<sup>4</sup> The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.



6 (bases 1 to 1699)  
**REFERENCE**  
**AUTHORS**  
 Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Boro,H., Carninci,P.,  
 Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,  
 Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,  
 Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,  
 Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,  
 Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,  
 Nakanura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,  
 Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,  
 Sano,H., Sasaki,D., Shibata,K., Shingawa,A., Shiraki,T.,  
 Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,  
 Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,  
 Yuramatsu,M. and Hayashizaki,Y.  
**TITLE**  
**JOURNAL**  
 Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of  
 Physical and Chemical Research (RIKEN), Laboratory for Genome  
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama,  
 Kanagawa 230-0045, Japan [E-mail: genome-resgsc.riken.go.jp,  
 URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,  
 Fax:81-45-503-9216]  
**COMMENT**  
 cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Please visit our web site for further details.  
 URL:http://genome.gsc.riken.go.jp/  
 URL:http://fantom.gsc.riken.go.jp/  
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## RESULT 7

AK028156 1701 bp mRNA linear HTC 18-SEP-2003  
Mus musculus adult male tongue cDNA, RIKEN full-length enriched  
library, clone:2310051P05 product:hypothetical Lipid-binding serum  
glycoprotein containing protein, full insert sequence.

## ACCESSION

AK028156.1 GI:26389741

## VERSION

HTC; CAP trapper.

## KEYWORDS

Mus musculus (house mouse)

## SOURCE

Mus musculus

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1 Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

99279253

PUBMED

10349636

## REFERENCE

2

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

20499374

PUBMED

11042159

## REFERENCE

3

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,

Konno, H., Akiyama, J., Nishi, K., Kitsumai, T., Tashiro, H., Itoh, M.,

Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,

Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,

Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,

Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,

Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer

Genome Res. 10 (11), 1757-1771 (2000)

20530913

PUBMED

11076861

## REFERENCE

4

The RIKEN Genome Exploration Research Group Phase II Team and the

PANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection

Nature 409, 685-690 (2001)

## REFERENCE

5

The PANTOM Consortium and the RIKEN Genome Exploration Research

Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 1701)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,











Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

Direct Submission  
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5'-GAGAGAGAGAGATCCAGAGCTCTTTTITTTTTTITVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'-GACAGAGAGATCTCGAGTTAATTAATATCCCCCCCCC 3'], cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.

Host: SOUR.

#### FEATURES

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Location/Qualifiers

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Matches 1095; Conservative 0; Mismatches 311; Indels 14; Gaps 4;

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[illegible]

RESULT 11

AK010157	AK010157	mRNA	1727 bp	linear	HTC 20-SEP-2003	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer
LOCUS						
DEFINITION						

AK01C154 1698 bp mRNA linear HTC 20-SEP-2003  
Mus musculus adult male tongue cDNA, RIKEN full-length enriched  
library, clone:2310074I02 product:hypothetical Lipid-binding serum  
glycoprotein containing protein, full insert sequence.

AK010154  
AK010154.1 GI:12845400  
HTC; CAP trapper.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
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Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.







them based on alignment.

FEATURES	SOURCE
1. <i>General</i>	
2. <i>Specific</i>	
3. <i>Other</i>	

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Best Local Similarity	73.3%	Pred. No. 7.1e-170		
Matches 999	Conservative	0	Mismatches 361	Indels 3
				Gaps 1

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QY	383	TTTTCGGAGTGGCGCTGCTGGCAGCAGCTAATTTTACTTTTCAAAGTCTTTTCGCGCCCCAGA	442
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DB	327	GCCCATGGAGCTGGTGTGTGCTGTAGACTTGTCTGGCTGATGTGCAGTGTGCCCGGGAGCTC	386
QY	503	CATCAGGACCCCTGTGTGTCAAGACTTCTGCTGCTCTTTATTTCTGGGGCCAGCCCAACGA	562
DB	387	TATTTGGACCCCTGTGTGTGAGGTCCCTGTGCTCTTCCATCTTCACTCCAGCCGGCAT	446
QY	563	GTTTGTGCGAGTAACAGCACCTCCACGCGCTGCTGGTCTGCTGGTGCAGGAAGCACATTA	622
DB	447	GCTGGATAGCAGTAACAGTACTCCAGGAGCTGCTCGACCGGGTGCAGGAGCACATCAA	506
QY	623	AGCTGTCTTTCAGATAACAAGCTGTGCCCTGAGCANCTCCAACTGGTGCAGGCTCAATGT	682
DB	507	AGTGTGACTTAAACAAAGCTGTCTTGCATGTCTATGGCTCTGGTCCAGGATCTCAATGT	566
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DB	627	CATPACAGCATGCCCAACCATCACAGTAACATATATATATATATATATATATATATATATAT	686
QY	803	CTTCTCTGTGGGCAAGCCCATCATCTCTGCCAG---GATGCCACCCCTTTTGTGTGGC	859
DB	687	CTCTCTCTTGTGGCAAAACCCATCTCTCTGCTCTATGCAATGTGTGTGTGTGTGTGTGTGT	746
QY	860	AAGGCAATGTGGGTACCGAGGGCTCCATGGCCACCGTGGGCCTCTCCACGAGCTGTTCGA	919
DB	747	ATGGCCCTTTGGGTGATGCAGGAGCCATGGCACTGTGGSGCTCTCCAGACCTGTITGA	806
QY	920	CTCTGTGCTCTCTGTGTGCAAGGCGGTGCCCTCAACCTGGACATCACAGGGCAGCT	979
DB	807	CTGTGTCCCTCTCTGATGCTT-CAGAAAGCTGTGCTCTCTCAACTGGAAATCACAGGGCAGCT	866
QY	980	GAGGTCCGATGACAACTCTGTGAAACCTCTGTCTGTGGCGCGGCTCTTCCCGAGGTGGC	1039
DB	867	GAATTCGAAAGAACATTCCTCTGAAACACCTCTGTGTGGCGCAGCTCATCCCTGAGTGGC	926





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 29, 2004, 10:59:00 ; Search time 49 Seconds  
(without alignments)  
2642.429 Million cell updates/sec

Title: US-10-069-034-28

Perfect score: 2265

Sequence: 1 MAWASRLGILLALLFPVGA.....PEIFVYGVYVSSGLFYQS 458

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1166195 seqs, 282705291 residues

Total number of hits satisfying chosen parameters: 1166195

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	DB ID	Description
1	2265	100.0	458	9 US-09-965-529-28
2	2265	100.0	458	10 US-09-969-680A-28
3	2265	100.0	458	15 US-10-291-265-350
4	2265	100.0	458	15 US-10-291-265-822
5	2260	99.8	458	12 US-10-206-915-498
6	2260	99.8	458	12 US-10-199-670-498
7	2260	99.8	458	12 US-10-201-858-498
8	2260	99.8	458	12 US-10-081-056-322
9	2260	99.8	458	12 US-10-203-890-498
10	2260	99.8	458	12 US-10-208-024-498
11	2260	99.8	458	12 US-10-201-853-498
12	2260	99.8	458	12 US-10-174-581-498
13	2260	99.8	458	12 US-10-176-483-498
14	2260	99.8	458	12 US-10-176-749-498
15	2260	99.8	458	12 US-10-176-914-498

16	2260	99.8	458	12	US-10-176-915-498	Sequence 498, App
17	2260	99.8	458	12	US-10-176-484-498	Sequence 498, App
18	2260	99.8	458	12	US-10-180-550-498	Sequence 498, App
19	2260	99.8	458	12	US-10-183-014-498	Sequence 498, App
20	2260	99.8	458	12	US-10-187-738-498	Sequence 498, App
21	2260	99.8	458	12	US-10-187-740-498	Sequence 498, App
22	2260	99.8	458	12	US-10-187-883-498	Sequence 498, App
23	2260	99.8	458	12	US-10-194-363-498	Sequence 498, App
24	2260	99.8	458	12	US-10-194-460-498	Sequence 498, App
25	2260	99.8	458	12	US-10-194-463-498	Sequence 498, App
26	2260	99.8	458	12	US-10-194-484-498	Sequence 498, App
27	2260	99.8	458	12	US-10-195-884-498	Sequence 498, App
28	2260	99.8	458	12	US-10-195-896-498	Sequence 498, App
29	2260	99.8	458	12	US-10-196-744-498	Sequence 498, App
30	2260	99.8	458	12	US-10-196-755-498	Sequence 498, App
31	2260	99.8	458	12	US-10-196-757-498	Sequence 498, App
32	2260	99.8	458	12	US-10-197-704-498	Sequence 498, App
33	2260	99.8	458	12	US-10-197-710-498	Sequence 498, App
34	2260	99.8	458	12	US-10-198-758-498	Sequence 498, App
35	2260	99.8	458	12	US-10-198-766-498	Sequence 498, App
36	2260	99.8	458	12	US-10-199-304-498	Sequence 498, App
37	2260	99.8	458	12	US-10-199-309-498	Sequence 498, App
38	2260	99.8	458	12	US-10-199-313-498	Sequence 498, App
39	2260	99.8	458	12	US-10-199-456-498	Sequence 498, App
40	2260	99.8	458	12	US-10-201-329-498	Sequence 498, App
41	2260	99.8	458	12	US-10-202-412-498	Sequence 498, App
42	2260	99.8	458	12	US-10-206-919-498	Sequence 498, App
43	2260	99.8	458	12	US-10-206-922-498	Sequence 498, App
44	2260	99.8	458	12	US-10-206-924-498	Sequence 498, App
45	2260	99.8	458	12	US-10-206-928-498	Sequence 498, App

#### ALIGNMENTS

RESULT 1  
US-09-965-529-28  
; Sequence 28, Application US/09965529  
; Publication No. US20020182671A1  
; GENERAL INFORMATION:  
; APPLICANT: LAL, Preeti  
; APPLICANT: YUE, Henry  
; APPLICANT: TANG, Y. Tom  
; APPLICANT: BANDMAN, Olga  
; APPLICANT: BURFORD, Neil  
; APPLICANT: AZIMZAI, Valda  
; APPLICANT: BAUGHN, Mariah R.  
; APPLICANT: LO, Dyrung Aina M.  
; APPLICANT: PATTERSON, Chandra  
; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS  
; FILE REFERENCE: PF-0731 USA  
; CURRENT APPLICATION NUMBER: US/09/965,529  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 60/164,203; PCT/US02/22315  
; PRIOR FILING DATE: 1999-08-17; 1999-11-09; 2000-08-14  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PERL Program  
; SEQ ID NO 28  
; LENGTH: 458  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20020182671A1 339343CD1  
US-09-965-529-28

Query Match 100.0%; Score 2265; DB 9; Length 458;  
Best Local Similarity 100.0%; Pred. No. 3e-209;  
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAWASRLGILLALLFPVGA...TGTVTVRLNKAALSYVSEIGKAPLQALQVTVPHLDWS 60  
DB 1 MAWASRLGILLALLFPVGA...TGTVTVRLNKAALSYVSEIGKAPLQALQVTVPHLDWS 60

```

QY 61 GEALQPTRIRILNVHVRHLKFIAGGVRLLAAANFTFKVFRAPPELETLFVELLADT 120
Db 61 GEALQPTRIRILNVHVRHLKFIAGGVRLLAAANFTFKVFRAPPELETLFVELLADT 120
QY 121 RVQSSIRTPVVISACSLFSGHANFDSNSTSHALLVLVQKHIAVLSNKLCLISINL 180
Db 121 RVQSSIRTPVVISACSLFSGHANFDSNSTSHALLVLVQKHIAVLSNKLCLISINL 180
QY 181 VQGVNHLGTLIGLNPVGPESQIRYSMVSVPTVTSYISLEVNNAVFLFLGKPIILPTDAT 240
Db 181 VQGVNHLGTLIGLNPVGPESQIRYSMVSVPTVTSYISLEVNNAVFLFLGKPIILPTDAT 240
QY 241 VQGVNHLGTLIGLNPVGPESQIRYSMVSVPTVTSYISLEVNNAVFLFLGKPIILPTDAT 240
Db 241 VQGVNHLGTLIGLNPVGPESQIRYSMVSVPTVTSYISLEVNNAVFLFLGKPIILPTDAT 240
QY 301 IPEVARQFPEPMPVVLKVRIGATPVAMLHTNNATLRLOPPFVEVLATASNSAFQSLFSLDV 360
Db 301 IPEVARQFPEPMPVVLKVRIGATPVAMLHTNNATLRLOPPFVEVLATASNSAFQSLFSLDV 360
QY 361 VVNRLQLSVSKVKGQITTSVLGDVQLTVASSNVGFIIDQVRLTGMGTVEKPELIDHLNA 420
Db 361 VVNRLQLSVSKVKGQITTSVLGDVQLTVASSNVGFIIDQVRLTGMGTVEKPELIDHLNA 420
QY 421 LLAMGIALPGVNLHVVAPEIFVYEGYVVISGLFYQS 458
Db 421 LLAMGIALPGVNLHVVAPEIFVYEGYVVISGLFYQS 458

```

## RESULT 2

```

US-09-969-680A-28
; Sequence 28, Application US/09969680A
; Publication No. US20030124649A1
; GENERAL INFORMATION:
; APPLICANT: LAL, Preeti; YUE, Henry
; APPLICANT: TANG, Y. Tom; SANDMAN, Olga
; APPLICANT: BURFORD, Neil; AZEMZAI, Yalda
; APPLICANT: BAUGHN, Maria R.; LU, Dyung Aina M.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
; FILE REFERENCE: PF-0731-1 USA
; CURRENT APPLICATION NUMBER: US/09/969,680A
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US00/22315
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/149,641
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/164,203
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 28
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20030124649A1 3393430CD1
US-09-969-680A-28

```

```

Query Match 100.0%; Score 2265; DB 10; Length 458;
Best Local Similarity 100.0%; Pred. No. 3e-209;
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAWASRLGLLLALLLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQALQVTPVPHFLDWS 60
Db 1 MAWASRLGLLLALLLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQALQVTPVPHFLDWS 60
QY 61 GEALQPTRIRILNVHVRHLKFIAGGVRLLAAANFTFKVFRAPPELETLFVELLADT 120
Db 61 GEALQPTRIRILNVHVRHLKFIAGGVRLLAAANFTFKVFRAPPELETLFVELLADT 120

```

```

QY 121 RVQSSIRTPVVISACSLFSGHANFDSNSTSHALLVLVQKHIAVLSNKLCLISINL 180
Db 121 RVQSSIRTPVVISACSLFSGHANFDSNSTSHALLVLVQKHIAVLSNKLCLISINL 180
QY 181 VQGVNHLGTLIGLNPVGPESQIRYSMVSVPTVTSYISLEVNNAVFLFLGKPIILPTDAT 240
Db 181 VQGVNHLGTLIGLNPVGPESQIRYSMVSVPTVTSYISLEVNNAVFLFLGKPIILPTDAT 240
QY 241 PFVLPVRHVTGEGSMATVGLSQQLFDSALLLQKAGALNLDITGQLRSDNNLNTSALGRL 300
Db 241 PFVLPVRHVTGEGSMATVGLSQQLFDSALLLQKAGALNLDITGQLRSDNNLNTSALGRL 300
QY 301 IPEVARQFPEPMPVVLKVRIGATPVAMLHTNNATLRLOPPFVEVLATASNSAFQSLFSLDV 360
Db 301 IPEVARQFPEPMPVVLKVRIGATPVAMLHTNNATLRLOPPFVEVLATASNSAFQSLFSLDV 360
QY 361 VVNRLQLSVSKVKGQITTSVLGDVQLTVASSNVGFIIDQVRLTGMGTVEKPELIDHLNA 420
Db 361 VVNRLQLSVSKVKGQITTSVLGDVQLTVASSNVGFIIDQVRLTGMGTVEKPELIDHLNA 420
QY 421 LLAMGIALPGVNLHVVAPEIFVYEGYVVISGLFYQS 458
Db 421 LLAMGIALPGVNLHVVAPEIFVYEGYVVISGLFYQS 458

```

## RESULT 3

```

US-10-291-265-350
; Sequence 350, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al
; TITLE OF INVENTION: No. US20030232054A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 350
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-350

```

```

Query Match 100.0%; Score 2265; DB 15; Length 458;
Best Local Similarity 100.0%; Pred. No. 3e-209;
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAWASRLGLLLALLLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQALQVTPVPHFLDWS 60
Db 1 MAWASRLGLLLALLLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQALQVTPVPHFLDWS 60
QY 61 GEALQPTRIRILNVHVRHLKFIAGGVRLLAAANFTFKVFRAPPELETLFVELLADT 120
Db 61 GEALQPTRIRILNVHVRHLKFIAGGVRLLAAANFTFKVFRAPPELETLFVELLADT 120
QY 121 RVQSSIRTPVVISACSLFSGHANFDSNSTSHALLVLVQKHIAVLSNKLCLISINL 180
Db 121 RVQSSIRTPVVISACSLFSGHANFDSNSTSHALLVLVQKHIAVLSNKLCLISINL 180
QY 181 VQGVNHLGTLIGLNPVGPESQIRYSMVSVPTVTSYISLEVNNAVFLFLGKPIILPTDAT 240
Db 181 VQGVNHLGTLIGLNPVGPESQIRYSMVSVPTVTSYISLEVNNAVFLFLGKPIILPTDAT 240
QY 241 PFVLPVRHVTGEGSMATVGLSQQLFDSALLLQKAGALNLDITGQLRSDNNLNTSALGRL 300

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Db 241 PFVLPVRHVTGEGMATVGL:SQOLFDSALLLLQKAGALNLDITGQLRSDNLLNTSALGRL 300  
QY 301 IPEVARQPEPMPVVLKVRGATPVAMLTHTNATLRLOPFVEVLATASNAFQSLFSLDV 360  
Db 301 IPEVARQPEPMPVVLKVRGATPVAMLTHTNATLRLOPFVEVLATASNAFQSLFSLDV 360  
QY 361 VVNLRLQLSVSKVKLGQTTSVLGDVQLTVASSNVGFIDTDQVRLTGMVTFEKLDELHNA 420  
Db 361 VVNLRLQLSVSKVKLGQTTSVLGDVQLTVASSNVGFIDTDQVRLTGMVTFEKLDELHNA 420  
QY 421 LLAMGIALPGVNLHYVAPEIFVYEGYVVISGLFYQS 458  
Db 421 LLAMGIALPGVNLHYVAPEIFVYEGYVVISGLFYQS 458

## RESULT 4

US-10-291-265-822  
; Sequence 822, Application US/10291265  
; Publication No. US20030232054A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; APPLICANT: Tagg et al  
; TITLE OF INVENTION: No. US20030232054A1el Nucleic Acids and Polypeptides  
; FILE REFERENCE: 21272-017 (785)  
; CURRENT APPLICATION NUMBER: US/10/291,265  
; CURRENT FILING DATE: 2000-01-25  
; PRIOR APPLICATION NUMBER: 09/491,404  
; PRIOR FILING DATE: 2000-01-25  
; PRIOR APPLICATION NUMBER: 09/617,746  
; PRIOR FILING DATE: 2000-07-17  
; PRIOR APPLICATION NUMBER: 09/631,451  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: 09/633,870  
; PRIOR FILING DATE: 2000-09-15  
; NUMBER OF SEQ ID NOS: 944  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 822  
; LENGTH: 458  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-291-265-822

Query Match 100.0%; Score 2265; DB 15; Length 458;  
Best Local Similarity 100.0%; Pred. No. 3e-209;  
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAWASRLGLLALLLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQALQVTPHFLDWS 60  
Db 1 MAWASRLGLLALLLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQALQVTPHFLDWS 60  
QY 61 GEALQPTRIRILNVHVRPLHLKFTAGFGVRLLAANFTFKVFRAPPELELTLPVELLADT 120  
Db 61 GEALQPTRIRILNVHVRPLHLKFTAGFGVRLLAANFTFKVFRAPPELELTLPVELLADT 120  
QY 121 RVTQSSIRTPVVISACSLFSGHANEFDCGNSSTSHALLVLVQKHIAVLSNKLCLISNL 180  
Db 121 RVTQSSIRTPVVISACSLFSGHANEFDCGNSSTSHALLVLVQKHIAVLSNKLCLISNL 180  
QY 181 VQGVNVHLGTLIGLNPVGPESQIRYSMVSVPTVSDYISLEVNVLFLGKPIILPTDAT 240  
Db 181 VQGVNVHLGTLIGLNPVGPESQIRYSMVSVPTVSDYISLEVNVLFLGKPIILPTDAT 240  
QY 241 PFVLPVRHVTGEGMATVGL:SQOLFDSALLLLQKAGALNLDITGQLRSDNLLNTSALGRL 300  
Db 241 PFVLPVRHVTGEGMATVGL:SQOLFDSALLLLQKAGALNLDITGQLRSDNLLNTSALGRL 300  
QY 301 IPEVARQPEPMPVVLKVRGATPVAMLTHTNATLRLOPFVEVLATASNAFQSLFSLDV 360  
Db 301 IPEVARQPEPMPVVLKVRGATPVAMLTHTNATLRLOPFVEVLATASNAFQSLFSLDV 360  
QY 361 VVNLRLQLSVSKVKLGQTTSVLGDVQLTVASSNVGFIDTDQVRLTGMVTFEKLDELHNA 420

Db 361 VVNLRLQLSVSKVKLGQTTSVLGDVQLTVASSNVGFIDTDQVRLTGMVTFEKLDELHNA 420  
QY 421 LLAMGIALPGVNLHYVAPEIFVYEGYVVISGLFYQS 458  
Db 421 LLAMGIALPGVNLHYVAPEIFVYEGYVVISGLFYQS 458

## RESULT 5

US-10-206-915-498  
; Sequence 498, Application US/10206915  
; Publication No. US20040029221A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3430RIC513  
; CURRENT APPLICATION NUMBER: US/10/206,915  
; CURRENT FILING DATE: 2002-07-26  
; PRIOR APPLICATION NUMBER: 10/052586  
; PRIOR FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059266  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063120  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063121  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063486  
; PRIOR FILING DATE: 1997-10-21  
; PRIOR APPLICATION NUMBER: 60/063540  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063541  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063544  
; PRIOR FILING DATE: 1997-10-28  
; Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 498  
; LENGTH: 458  
; TYPE: PRT  
; ORGANISM: Homo Sapien

US-10-206-915-498

Query Match 99.8%; Score 2260; DB 12; Length 458;  
Best Local Similarity 99.8%; Pred. No. 9.2e-209;  
Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAWASRLGLLALLLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQALQVTPHFLDWS 60  
Db 1 MAWASRLGLLALLLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQALQVTPHFLDWS 60  
QY 61 GEALQPTRIRILNVHVRPLHLKFTAGFGVRLLAANFTFKVFRAPPELELTLPVELLADT 120  
Db 61 GEALQPTRIRILNVHVRPLHLKFTAGFGVRLLAANFTFKVFRAPPELELTLPVELLADT 120  
QY 121 RVTQSSIRTPVVISACSLFSGHANEFDCGNSSTSHALLVLVQKHIAVLSNKLCLISNL 180  
Db 121 RVTQSSIRTPVVISACSLFSGHANEFDCGNSSTSHALLVLVQKHIAVLSNKLCLISNL 180  
QY 181 VQGVNVHLGTLIGLNPVGPESQIRYSMVSVPTVSDYISLEVNVLFLGKPIILPTDAT 240

Db 181 VQSVNHLGLTLGLNPGVSGQIRYSWVSPTVTSYISLEVNVLFLGLNPIILPTDAT 240  
QY 241 PFVLPRLHVGTGEGSMATVGLSQQLFDSALLLQKAGALNLDITGQLRSDNLLNTSALGRL 300  
Db 241 PFVLPRLHVGTGEGSMATVGLSQQLFDSALLLQKAGALNLDITGQLRSDNLLNTSALGRL 300  
QY 301 IPEVARQPEPMPVVLKVLGATPVAMLHTNNATLRLQPFVEVLATASNSAFQSLFSLDV 360  
Db 301 IPEVARQPEPMPVVLKVLGATPVAMLHTNNATLRLQPFVEVLATASNSAFQSLFSLDV 360  
QY 361 VVNRLQLSVSKVQLGTTSLVGLDVOLTVAASNVGFDITDQVRLMGTVFEKPLDLHLNA 420  
Db 361 VVNRLQLSVSKVQLGTTSLVGLDVOLTVAASNVGFDITDQVRLMGTVFEKPLDLHLNA 420  
QY 421 LLAMGIALPGVNVHLHYVAPEIFVYEGYVVISGLFYQS 458  
Db 421 LLAMGIALPGVNVHLHYVAPEIFVYEGYVVISGLFYQS 458

## RESULT 6

US-10-199-670-498  
; Sequence 498, Application US/10199670  
; Publication No. US20040033560A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Goddard, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430R1C401  
; CURRENT APPLICATION NUMBER: US/10/199,670  
; CURRENT FILING DATE: 2002-07-19  
; PRIOR APPLICATION NUMBER: 10/052586  
; PRIOR FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059266  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063120  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063121  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063486  
; PRIOR FILING DATE: 1997-10-21  
; PRIOR APPLICATION NUMBER: 60/063540  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063541  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063544  
; PRIOR FILING DATE: 1997-10-28  
; Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 498  
; LENGTH: 458  
; TYPE: PRT  
; ORGANISM: Homo Sapien

US-10-199-670-498

Query Match 99.8%; Score 2260; DB 12; Length 458;  
Best Local Similarity 99.8%; Freq. No. 9.2e-209;  
Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAWASRLGLLLALLLPVCGASTPGTVVRLNKAALSYVSEIGKAPLQALQVTPVPHFLDWS 60  
Db 1 MAWASRLGLLLALLLPVCGASTPGTVVRLNKAALSYVSEIGKAPLQALQVTPVPHFLDWS 60  
QY 61 GHALQPTRIRIILNVHVRHLKPIAGFGVRLILAAANFTPKVFRAPPELETLTPVELLIADT 120  
Db 61 GHALQPTRIRIILNVHVRHLKPIAGFGVRLILAAANFTPKVFRAPPELETLTPVELLIADT 120  
QY 121 RVTQSSIRTPVVISIACSLFSGHANEFDSNSTSHALLVLVOKHIAVLSNK-CLISISNL 180  
Db 121 RVTQSSIRTPVVISIACSLFSGHANEFDSNSTSHALLVLVOKHIAVLSNK-CLISISNL 180  
QY 181 VQSVNHLGLTLGLNPGVSGQIRYSWVSPTVTSYISLEVNVLFLGLNPIILPTDAT 240  
Db 181 VQSVNHLGLTLGLNPGVSGQIRYSWVSPTVTSYISLEVNVLFLGLNPIILPTDAT 240  
QY 241 PFVLPRLHVGTGEGSMATVGLSQQLFDSALLLQKAGALNLDITGQLRSDNLLNTSALGRL 300  
Db 241 PFVLPRLHVGTGEGSMATVGLSQQLFDSALLLQKAGALNLDITGQLRSDNLLNTSALGRL 300  
QY 301 IPEVARQPEPMPVVLKVLGATPVAMLHTNNATLRLQPFVEVLATASNSAFQSLFSLDV 360  
Db 301 IPEVARQPEPMPVVLKVLGATPVAMLHTNNATLRLQPFVEVLATASNSAFQSLFSLDV 360  
QY 361 VVNRLQLSVSKVQLGTTSLVGLDVOLTVAASNVGFDITDQVRLMGTVFEKPLDLHLNA 420  
Db 361 VVNRLQLSVSKVQLGTTSLVGLDVOLTVAASNVGFDITDQVRLMGTVFEKPLDLHLNA 420  
QY 421 LLAMGIALPGVNVHLHYVAPEIFVYEGYVVISGLFYQS 458  
Db 421 LLAMGIALPGVNVHLHYVAPEIFVYEGYVVISGLFYQS 458

## RESULT 7

US-10-201-858-498  
; Sequence 498, Application US/10201858  
; Publication No. US20040038337A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430R1C464  
; CURRENT APPLICATION NUMBER: US/10/201,858  
; CURRENT FILING DATE: 2002-07-23  
; PRIOR APPLICATION NUMBER: 10/052586  
; PRIOR FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059266  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063120  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063121  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063486  
; PRIOR FILING DATE: 1997-10-21  
; PRIOR APPLICATION NUMBER: 60/063540  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063541  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063544

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; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; SEQ ID NO 498
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-201-858-498

Query Match          99.8%; Score 2260; DB 12; Length 458;
Best Local Similarity 99.8%; Pred. No. 9.2e-209;
Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAWASRLGALLLPVVGASTPGTWRINKAALSYSVSEIGKAPLQALQVTVRFLDWS 60
DB 1 MAWASRLGALLLPVVGASTPGTWRINKAALSYSVSEIGKAPLQALQVTVRFLDWS 60
QY 61 GEALQPTIRILNVHVRHLKFIAGFVRLAAANFTFKVFRAPPELELTLPVELLADT 120
DB 61 GEALQPTIRILNVHVRHLKFIAGFVRLAAANFTFKVFRAPPELELTLPVELLADT 120
QY 121 RVTOSSIRTPVVISACSLFSGHANEFDSNSTSHALLVWQKHKAVLSNKLCLISNL 180
DB 121 RVTOSSIRTPVVISACSLFSGHANEFDSNSTSHALLVWQKHKAVLSNKLCLISNL 180
QY 181 VQGVNVHGLTILGNPVPSPESQIRYSMSVPTVTSYISLEVNVLFLILKPIILPTDAT 240
DB 181 VQGVNVHGLTILGNPVPSPESQIRYSMSVPTVTSYISLEVNVLFLILKPIILPTDAT 240
QY 241 PFVLPVRHVTGSMATVGSQOLFPSALLLQKAGALNDITQGRSDNLTNTSALGRL 300
DB 241 PFVLPVRHVTGSMATVGSQOLFPSALLLQKAGALNDITQGRSDNLTNTSALGRL 300
QY 301 IPEVARQPEBPMPVVLKVLGATPVMHLHTNATLROPEVEVLATANSAPQSFSLDV 360
DB 301 IPEVARQPEBPMPVVLKVLGATPVMHLHTNATLROPEVEVLATANSAPQSFSLDV 360
QY 361 VVNLRLQLSVSKVKLQGTTSVLGDVQLVASSNVGFIIDTQVRLTGMVTFEKLPHLHNA 420
DB 361 VVNLRLQLSVSKVKLQGTTSVLGDVQLVASSNVGFIIDTQVRLTGMVTFEKLPHLHNA 420
QY 421 LLANGIALPGVNVHLHYVAPEIFVVEGYVVISGLFPYQS 458
DB 421 LLANGIALPGVNVHLHYVAPEIFVVEGYVVISGLFPYQS 458

RESULT 8
US-10-081-056-322
; Sequence 322, Application US/10081056
; Publication No. US20040043927A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235PLC1
; CURRENT APPLICATION NUMBER: US/10/081.056
; CURRENT FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: PCT/US01/21735
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; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/230,978
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/000,000
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 09/664,610
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/242,922
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 09/709,238
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: PCT/US00/30952
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/747,259
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 09/767,609
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: US 09/796,498
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06666
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: US 09/802,706
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US 09/808,689
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 09/816,744
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 09/828,366
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 09/854,208
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/854,280
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 09/866,034
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/US01/17092
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 09/870,574
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US01/17443
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
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; PRIOR APPLICATION NUMBER: PCT/US01/00000
; PRIOR FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 322
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homosapiens
US-10-081-056-322

Query Match          99.8%; Score 2260; DB 12; Length 458;
Best Local Similarity 99.8%; Pred. No. 9.2e-209;
Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAWASRLGLALLLPVVGASTPGTVRLNKAALSVVSEIGKAPLQALQVTVPHFLDWS 60
Db 1 MAWASRLGLALLLPVVGASTPGTVRLNKAALSVVSEIGKAPLQALQVTVPHFLDWS 60
QY 61 GEALQPTRIRILNVHVRHLKFIAGGVRLLAANFTKVFRAPELELTLPVELLADT 120
Db 61 GEALQPTRIRILNVHVRHLKFIAGGVRLLAANFTKVFRAPELELTLPVELLADT 120
QY 121 RVQSSIRTPVWSISACSLFSGHANEFDGNSNSTSHALLVLVQKHKAVLSNKLCLISNL 180
Db 121 RVQSSIRTPVWSISACSLFSGHANEFDGNSNSTSHALLVLVQKHKAVLSNKLCLISNL 180
QY 181 VQGVNHLGTLGLNPVGPESQIRYSMVSVPTVTSYISLEVNNAVFLGKPIILPTDAT 240
Db 181 VQGVNHLGTLGLNPVGPESQIRYSMVSVPTVTSYISLEVNNAVFLGKPIILPTDAT 240
QY 241 PFVLPVHVTGEGSMATVGLSQQLFDSALLLQKAGALNLDITGQLSDNLLNTSALGRL 300
Db 241 PFVLPVHVTGEGSMATVGLSQQLFDSALLLQKAGALNLDITGQLSDNLLNTSALGRL 300
QY 301 IPEVARQFPEPMPVVLKVLGATPVAMLHTNNATLRLQPPFVEVLATASNSAFQSLFSDV 360
Db 301 IPEVARQFPEPMPVVLKVLGATPVAMLHTNNATLRLQPPFVEVLATASNSAFQSLFSDV 360
QY 361 VVNLRLQLSVSKVKGTTSLVGDVQLTVASSNVGFIIDQVRLMGTVFEKPLLDHLNA 420
Db 361 VVNLRLQLSVSKVKGTTSLVGDVQLTVASSNVGFIIDQVRLMGTVFEKPLLDHLNA 420
QY 421 LLAMGIALPGVNLHVVAPEIFVYEGYVVISGLFYQS 458
Db 421 LLAMGIALPGVNLHVVAPEIFVYEGYVVISGLFYQS 458

RESULT 9
US-10-205-890-498
; Sequence 498, Application US/10205890
; Publication No. US20040048334A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430RIC519
; CURRENT APPLICATION NUMBER: US/10/205,890
; PRIOR FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 63/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
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; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 498
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-205-890-498

Query Match          99.8%; Score 2260; DB 12; Length 458;
Best Local Similarity 99.8%; Pred. No. 9.2e-209;
Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAWASRLGLALLLPVVGASTPGTVRLNKAALSVVSEIGKAPLQALQVTVPHFLDWS 60
Db 1 MAWASRLGLALLLPVVGASTPGTVRLNKAALSVVSEIGKAPLQALQVTVPHFLDWS 60
QY 61 GEALQPTRIRILNVHVRHLKFIAGGVRLLAANFTKVFRAPELELTLPVELLADT 120
Db 61 GEALQPTRIRILNVHVRHLKFIAGGVRLLAANFTKVFRAPELELTLPVELLADT 120
QY 121 RVQSSIRTPVWSISACSLFSGHANEFDGNSNSTSHALLVLVQKHKAVLSNKLCLISNL 180
Db 121 RVQSSIRTPVWSISACSLFSGHANEFDGNSNSTSHALLVLVQKHKAVLSNKLCLISNL 180
QY 181 VQGVNHLGTLGLNPVGPESQIRYSMVSVPTVTSYISLEVNNAVFLGKPIILPTDAT 240
Db 181 VQGVNHLGTLGLNPVGPESQIRYSMVSVPTVTSYISLEVNNAVFLGKPIILPTDAT 240
QY 241 PFVLPVHVTGEGSMATVGLSQQLFDSALLLQKAGALNLDITGQLSDNLLNTSALGRL 300
Db 241 PFVLPVHVTGEGSMATVGLSQQLFDSALLLQKAGALNLDITGQLSDNLLNTSALGRL 300
QY 301 IPEVARQFPEPMPVVLKVLGATPVAMLHTNNATLRLQPPFVEVLATASNSAFQSLFSDV 360
Db 301 IPEVARQFPEPMPVVLKVLGATPVAMLHTNNATLRLQPPFVEVLATASNSAFQSLFSDV 360
QY 361 VVNLRLQLSVSKVKGTTSLVGDVQLTVASSNVGFIIDQVRLMGTVFEKPLLDHLNA 420
Db 361 VVNLRLQLSVSKVKGTTSLVGDVQLTVASSNVGFIIDQVRLMGTVFEKPLLDHLNA 420
QY 421 LLAMGIALPGVNLHVVAPEIFVYEGYVVISGLFYQS 458
Db 421 LLAMGIALPGVNLHVVAPEIFVYEGYVVISGLFYQS 458

RESULT 10
US-10-208-024-498
; Sequence 498, Application US/10208024
; Publication No. US20040048335A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
```

APPLICANT: Wood,William I.  
APPLICANT: Zhang,Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3430RIC538  
CURRENT APPLICATION NUMBER: US/10/208,024  
CURRENT FILING DATE: 2002-07-29  
PRIOR APPLICATION NUMBER: 10/052586  
PRIOR FILING DATE: 2002-01-15  
PRIOR APPLICATION NUMBER: 60/059263  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/059266  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063120  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063121  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063486  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063541  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063544  
PRIOR FILING DATE: 1997-10-28  
PRIOR Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 612  
SEQ ID NO 498  
LENGTH: 458  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-208-024-498

Query Match 99.8%; Score 2260; DB 12; Length 458;  
Best Local Similarity 99.8%; Pred. No. 9.2e-209;  
Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MAWASRLGLLLALLPVVGASTPGTIVRLNKAAALSVSEIGKAPLQALQVTPHFLDWS 60  
DB 1 MAWASRLGLLLALLPVVGASTPGTIVRLNKAAALSVSEIGKAPLQALQVTPHFLDWS 60  
QY 61 GEALQPTRIRILNVHVRHLKFIAGFGVRLAAANFTKVFRAPEPLTLPEVLLADT 120  
DB 61 GEALQPTRIRILNVHVRHLKFIAGFGVRLAAANFTKVFRAPEPLTLPEVLLADT 120  
QY 121 RVTQSSIRTPVVISACSLFSGHANEFDCGNSNSTSHALLVQKHKAVLSNKLCLISNLS 180  
DB 121 RVTQSSIRTPVVISACSLFSGHANEFDCGNSNSTSHALLVQKHKAVLSNKLCLISNLS 180  
QY 181 VQGVNVHLGTLIGLNPVGPESQIRYSMSVPTVTSYISLEVNVLFLGKPIILPTDAT 240  
DB 181 VQGVNVHLGTLIGLNPVGPESQIRYSMSVPTVTSYISLEVNVLFLGKPIILPTDAT 240  
QY 241 PFVLPFRHVGTGSMATVGLSQOLFDSALLLQKAGALNLDITGQRRSDNLTNTSALGRL 300  
DB 241 PFVLPFRHVGTGSMATVGLSQOLFDSALLLQKAGALNLDITGQRRSDNLTNTSALGRL 300  
QY 301 IPEVARQPEPMPVVLKVRGATPVAMLHTNNTLRLOPFVEVLATASNSAFQSLFSLDV 360  
DB 301 IPEVARQPEPMPVVLKVRGATPVAMLHTNNTLRLOPFVEVLATASNSAFQSLFSLDV 360  
QY 361 VVNLRLQLSVKVKLQGTTSVLGDVQLTVASSNVGFIDTQVRLMGTVFEXPLDLHNA 420  
DB 361 VVNLRLQLSVKVKLQGTTSVLGDVQLTVASSNVGFIDTQVRLMGTVFEXPLDLHNA 420  
QY 421 LLAMGIALPGVNLHYVAPEIFVYEGYVVISGLFYQS 458  
DB 421 LLAMGIALPGVNLHYVAPEIFVYEGYVVISGLFYQS 458

RESULT 11

US-10-201-853-498  
Sequence 498, Application US/10201853  
Publication No. US20040053358A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Chen, Jian  
APPLICANT: Desnoyers, Luc  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Pan, James  
APPLICANT: Smith, Victoria  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3430RIC465  
CURRENT APPLICATION NUMBER: US/10/201,853  
CURRENT FILING DATE: 2002-07-23  
PRIOR APPLICATION NUMBER: 10/052586  
PRIOR FILING DATE: 2002-01-15  
PRIOR APPLICATION NUMBER: 60/059263  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/059266  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063120  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063121  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063486  
PRIOR FILING DATE: 1997-10-21  
PRIOR APPLICATION NUMBER: 60/063540  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063541  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063544  
PRIOR Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 612  
SEQ ID NO 498  
LENGTH: 458  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-201-853-498

Query Match 99.8%; Score 2260; DB 12; Length 458;  
Best Local Similarity 99.8%; Pred. No. 9.2e-209;  
Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MAWASRLGLLLALLPVVGASTPGTIVRLNKAAALSVSEIGKAPLQALQVTPHFLDWS 60  
DB 1 MAWASRLGLLLALLPVVGASTPGTIVRLNKAAALSVSEIGKAPLQALQVTPHFLDWS 60  
QY 61 GEALQPTRIRILNVHVRHLKFIAGFGVRLAAANFTKVFRAPEPLTLPEVLLADT 120  
DB 61 GEALQPTRIRILNVHVRHLKFIAGFGVRLAAANFTKVFRAPEPLTLPEVLLADT 120  
QY 121 RVTQSSIRTPVVISACSLFSGHANEFDCGNSNSTSHALLVQKHKAVLSNKLCLISNLS 180  
DB 121 RVTQSSIRTPVVISACSLFSGHANEFDCGNSNSTSHALLVQKHKAVLSNKLCLISNLS 180  
QY 181 VQGVNVHLGTLIGLNPVGPESQIRYSMSVPTVTSYISLEVNVLFLGKPIILPTDAT 240  
DB 181 VQGVNVHLGTLIGLNPVGPESQIRYSMSVPTVTSYISLEVNVLFLGKPIILPTDAT 240  
QY 241 PFVLPFRHVGTGSMATVGLSQOLFDSALLLQKAGALNLDITGQRRSDNLTNTSALGRL 300  
DB 241 PFVLPFRHVGTGSMATVGLSQOLFDSALLLQKAGALNLDITGQRRSDNLTNTSALGRL 300  
QY 301 IPEVARQPEPMPVVLKVRGATPVAMLHTNNTLRLOPFVEVLATASNSAFQSLFSLDV 360

Db 301 IPEVAQFPEFWLKVRLGATPVAMLHTNATLRLQPFVEVLATASAFOSLSFLDV 360  
QY 361 VVNRLQLSVKVKLQTTSLVGLDVLTASSVNGFIDTDQVRLMGTFVEKPLLDHNA 420  
Db 361 VVNRLQLSVKVKLQTTSLVGLDVLTASSVNGFIDTDQVRLMGTFVEKPLLDHNA 420  
QY 421 LLAMGIALPGVNLHVAPFIYEGVWVSSGLFYQS 458  
Db 421 LLAMGIALPGVNLHVAPFIYEGVWVSSGLFYQS 458

RESULT 12  
US-10-174-581-498  
? Sequence 498, Application US/10174581  
? Publication No. US20030017540A1  
? GENERAL INFORMATION:  
? APPLICANT: Baker, Kevin P.  
? APPLICANT: Chen, Jian  
? APPLICANT: Destroers, Luc  
? APPLICANT: Goddard, Audrey  
? APPLICANT: Godowski, Paul J.  
? APPLICANT: Gurney, Austin L.  
? APPLICANT: Pan, James  
? APPLICANT: Smith, Victoria  
? APPLICANT: Watanabe, Colin K.  
? APPLICANT: Wood, William I.  
? APPLICANT: Zhang, Zemin  
? TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
? FILE REFERENCE: P3430R1C41  
? CURRENT APPLICATION NUMBER: US/10/174,581  
? CURRENT FILING DATE: 2002-06-18  
? PRIOR APPLICATION NUMBER: 10/0522586  
? PRIOR FILING DATE: 2002-01-15  
? PRIOR APPLICATION NUMBER: 60/059263  
? PRIOR FILING DATE: 1997-09-18  
? PRIOR APPLICATION NUMBER: 60/059266  
? PRIOR FILING DATE: 1997-09-18  
? PRIOR APPLICATION NUMBER: 60/062250  
? PRIOR FILING DATE: 1997-10-17  
? PRIOR APPLICATION NUMBER: 60/063120  
? PRIOR FILING DATE: 1997-10-24  
? PRIOR APPLICATION NUMBER: 60/063121  
? PRIOR FILING DATE: 1997-10-24  
? PRIOR APPLICATION NUMBER: 60/063486  
? PRIOR FILING DATE: 1997-10-21  
? PRIOR APPLICATION NUMBER: 60/063540  
? PRIOR FILING DATE: 1997-10-28  
? PRIOR APPLICATION NUMBER: 60/063541  
? PRIOR FILING DATE: 1997-10-28  
? PRIOR APPLICATION NUMBER: 60/063544  
? PRIOR FILING DATE: 1997-10-28  
? PRIOR APPLICATION NUMBER: 60/063564  
? PRIOR FILING DATE: 1997-10-28  
? PRIOR APPLICATION NUMBER: 60/063734  
? PRIOR FILING DATE: 1997-10-29  
? PRIOR APPLICATION NUMBER: 60/063870  
? PRIOR FILING DATE: 1997-10-31  
? PRIOR APPLICATION NUMBER: 60/064103  
? PRIOR FILING DATE: 1997-10-31  
? PRIOR APPLICATION NUMBER: 60/065311  
? PRIOR FILING DATE: 1997-11-13  
? PRIOR APPLICATION NUMBER: 60/066120  
? PRIOR FILING DATE: 1997-11-21  
? PRIOR APPLICATION NUMBER: 60/066466  
? PRIOR FILING DATE: 1997-11-24  
? PRIOR APPLICATION NUMBER: 60/066772  
? PRIOR FILING DATE: 1997-11-24  
? PRIOR APPLICATION NUMBER: 60/069335  
? PRIOR FILING DATE: 1997-12-11  
? PRIOR APPLICATION NUMBER: 60/069425  
? PRIOR FILING DATE: 1997-12-12

? PRIOR APPLICATION NUMBER: 60/069870  
? PRIOR FILING DATE: 1997-12-17  
? PRIOR APPLICATION NUMBER: 60/068017  
? PRIOR FILING DATE: 1997-12-18  
? PRIOR APPLICATION NUMBER: 60/077450  
? PRIOR FILING DATE: 1998-03-10  
? PRIOR APPLICATION NUMBER: 60/077632  
? PRIOR FILING DATE: 1998-03-11  
? PRIOR APPLICATION NUMBER: 60/077649  
? PRIOR FILING DATE: 1998-03-11  
? PRIOR APPLICATION NUMBER: 60/078886  
? PRIOR FILING DATE: 1998-03-20  
? PRIOR APPLICATION NUMBER: 60/078939  
? PRIOR FILING DATE: 1998-03-20  
? PRIOR APPLICATION NUMBER: 60/079664  
? PRIOR FILING DATE: 1998-03-27  
? PRIOR APPLICATION NUMBER: 60/079786  
? PRIOR FILING DATE: 1998-03-27  
? PRIOR APPLICATION NUMBER: 60/080107  
? PRIOR FILING DATE: 1998-03-31  
? PRIOR APPLICATION NUMBER: 60/080194  
? PRIOR FILING DATE: 1998-03-31  
? PRIOR APPLICATION NUMBER: 60/080327  
? PRIOR FILING DATE: 1998-04-01  
? PRIOR APPLICATION NUMBER: 60/080333  
? PRIOR FILING DATE: 1998-04-01  
? PRIOR APPLICATION NUMBER: 60/081049  
? PRIOR FILING DATE: 1998-04-08  
? PRIOR APPLICATION NUMBER: 60/081070  
? PRIOR FILING DATE: 1998-04-08  
? PRIOR APPLICATION NUMBER: 60/081195  
? PRIOR FILING DATE: 1998-04-09  
? PRIOR APPLICATION NUMBER: 60/081838  
? PRIOR FILING DATE: 1998-04-15  
? PRIOR APPLICATION NUMBER: 60/082568  
? PRIOR FILING DATE: 1998-04-21  
? PRIOR APPLICATION NUMBER: 60/082569  
? PRIOR FILING DATE: 1998-04-21  
? PRIOR APPLICATION NUMBER: 60/082704  
? PRIOR FILING DATE: 1998-04-22  
? PRIOR APPLICATION NUMBER: 60/082797  
? PRIOR FILING DATE: 1998-04-22  
? PRIOR APPLICATION NUMBER: 60/083322  
? PRIOR FILING DATE: 1998-04-28  
? PRIOR APPLICATION NUMBER: 60/083495  
? PRIOR FILING DATE: 1998-04-29  
? PRIOR APPLICATION NUMBER: 60/083496  
? PRIOR FILING DATE: 1998-04-29  
? PRIOR APPLICATION NUMBER: 60/083499  
? PRIOR FILING DATE: 1998-04-29  
? PRIOR APPLICATION NUMBER: 60/083559  
? PRIOR FILING DATE: 1998-04-29  
? PRIOR APPLICATION NUMBER: 60/084366  
? PRIOR FILING DATE: 1998-05-05  
? PRIOR APPLICATION NUMBER: 60/084414  
? PRIOR FILING DATE: 1998-05-06  
? PRIOR APPLICATION NUMBER: 60/084639  
? PRIOR FILING DATE: 1998-05-07  
? PRIOR APPLICATION NUMBER: 60/084640  
? PRIOR FILING DATE: 1998-05-07  
? PRIOR APPLICATION NUMBER: 60/084643  
? PRIOR FILING DATE: 1998-05-07  
? PRIOR APPLICATION NUMBER: 60/085573  
? PRIOR FILING DATE: 1998-05-15  
? PRIOR APPLICATION NUMBER: 60/085579  
? PRIOR FILING DATE: 1998-05-15  
? PRIOR APPLICATION NUMBER: 60/085580  
? PRIOR FILING DATE: 1998-05-15  
? PRIOR APPLICATION NUMBER: 60/085582  
? PRIOR FILING DATE: 1998-05-15  
? PRIOR APPLICATION NUMBER: 60/085700  
? PRIOR FILING DATE: 1998-05-15  
? PRIOR APPLICATION NUMBER: 60/086023

;; PRIOR FILING DATE: 1998-05-18  
;; PRIOR APPLICATION NUMBER: 60/086392  
;; PRIOR FILING DATE: 1998-05-22  
;; PRIOR APPLICATION NUMBER: 60/086486  
;; PRIOR FILING DATE: 1998-05-22  
;; PRIOR APPLICATION NUMBER: 60/087098  
;; PRIOR FILING DATE: 1998-05-28  
;; PRIOR APPLICATION NUMBER: 60/087208  
;; PRIOR FILING DATE: 1998-05-28  
;; PRIOR APPLICATION NUMBER: 60/087603  
;; PRIOR FILING DATE: 1998-06-02  
;; PRIOR APPLICATION NUMBER: 60/087759  
;; PRIOR FILING DATE: 1998-06-02  
;; PRIOR APPLICATION NUMBER: 60/087827  
;; PRIOR FILING DATE: 1998-06-03  
;; PRIOR APPLICATION NUMBER: 60/088025  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088028  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088029  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088033  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088167  
;; PRIOR FILING DATE: 1998-06-05  
;; PRIOR APPLICATION NUMBER: 60/088202  
;; PRIOR FILING DATE: 1998-06-05  
;; PRIOR APPLICATION NUMBER: 60/088212  
;; PRIOR FILING DATE: 1998-06-05  
;; PRIOR APPLICATION NUMBER: 60/088217  
;; PRIOR FILING DATE: 1998-06-05  
;; PRIOR APPLICATION NUMBER: 60/088326  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088655  
;; PRIOR FILING DATE: 1998-06-09  
;; PRIOR APPLICATION NUMBER: 60/088722  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088738  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088824  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088825  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088826  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088861  
;; PRIOR FILING DATE: 1998-06-11  
;; PRIOR APPLICATION NUMBER: 60/088863  
;; PRIOR FILING DATE: 1998-06-11  
;; PRIOR APPLICATION NUMBER: 60/088876  
;; PRIOR FILING DATE: 1998-06-11  
;; PRIOR APPLICATION NUMBER: 60/089090  
;; PRIOR FILING DATE: 1998-06-12  
;; PRIOR APPLICATION NUMBER: 60/089105  
;; PRIOR FILING DATE: 1998-06-12  
;; PRIOR APPLICATION NUMBER: 60/089512  
;; PRIOR FILING DATE: 1998-06-15  
;; PRIOR APPLICATION NUMBER: 60/089514  
;; PRIOR FILING DATE: 1998-06-16  
;; PRIOR APPLICATION NUMBER: 60/089538  
;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089598  
;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089653

Query Match 99.8%; Score 2260; DB 12; Length 458;  
Best Local Similarity 99.8%; Pred. No. 9.2e-209;  
Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAWASRLGLLLALLLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQALQVTVPHFLDWS 60  
DB 1 MAWASRLGLLLALLLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQALQVTVPHFLDWS 60  
QY 61 GEALQPTIRILNVHVPRLHLKFIAGFGVRLAAANFTFKVFRAPPELELTPVELLADT 120  
DB 61 GEALQPTIRILNVHVPRLHLKFIAGFGVRLAAANFTFKVFRAPPELELTPVELLADT 120  
QY 121 RVTQSSIRTPVWSISACSLFSGHANEPDGSNSTSHALLVLVQKHKAVLSNKLCLISINL 180  
DB 121 RVTQSSIRTPVWSISACSLFSGHANEPDGSNSTSHALLVLVQKHKAVLSNKLCLISINL 180  
QY 181 VQGVNHLGLTGLGNPVPESQIRYSVMVSVTVTSYISLEVNVLFLGNPILPTDAT 240  
DB 181 VQGVNHLGLTGLGNPVPESQIRYSVMVSVTVTSYISLEVNVLFLGNPILPTDAT 240  
QY 241 PFVLPRHVGTGEGSMATVGLSQOLFDSALLLQKAGALNLDITGOLRSDDNLTNTSALGRL 300  
DB 241 PFVLPRHVGTGEGSMATVGLSQOLFDSALLLQKAGALNLDITGOLRSDDNLTNTSALGRL 300  
QY 301 IPEVARQFPPEMPVVLKVRIGATPVAMLHTNNATRLQPFVEVLATASNSAFQSLFSLDV 360  
DB 301 IPEVARQFPPEMPVVLKVRIGATPVAMLHTNNATRLQPFVEVLATASNSAFQSLFSLDV 360  
QY 361 VVNLRLQLSYKVKLQGTTSVLGDVQLTVASSNVGFIQDQVRLMGTVFKEPILDLHNA 420  
DB 361 VVNLRLQLSYKVKLQGTTSVLGDVQLTVASSNVGFIQDQVRLMGTVFKEPILDLHNA 420  
QY 421 LLAMGIALPGVNLHYVAPEIFVYEGYVWISSGLFYQS 458  
DB 421 LLAMGIALPGVNLHYVAPEIFVYEGYVWISSGLFYQS 458

## RESULT 13

US-10-176-483-498  
; Sequence 498, Application US/10176483  
; Publication No. US20030017541A1

## GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3430RIC68  
; CURRENT APPLICATION NUMBER: US/10/176,483  
; CURRENT FILING DATE: 2002-06-20  
; Prior application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 498  
; LENGTH: 458  
; TYPE: PRT  
; ORGANISM: Homo Sapien

US-10-176-483-498

Query Match 99.8%; Score 2260; DB 12; Length 458;  
Best Local Similarity 99.8%; Pred. No. 9.2e-209;  
Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAWASRLGLLLALLLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQALQVTVPHFLDWS 60  
DB 1 MAWASRLGLLLALLLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQALQVTVPHFLDWS 60  
QY 61 GEALQPTIRILNVHVPRLHLKFIAGFGVRLAAANFTFKVFRAPPELELTPVELLADT 120  
DB 61 GEALQPTIRILNVHVPRLHLKFIAGFGVRLAAANFTFKVFRAPPELELTPVELLADT 120

QY 121 RVTQSSIRTPVWSISACSLFSGHANEDGSGNSTSHALLVLVQKHKAVLSNKLCLISNL 180  
Db 121 RVTQSSIRTPVWSISACSLFSGHANEDGSGNSTSHALLVLVQKHKAVLSNKLCLISNL 180  
QY 181 VQGVNHLGTLIGLNPVGPESQIRYSMVSVPTVTSYISLEVNALVFLGKPIILPTDAT 240  
Db 181 VQGVNHLGTLIGLNPVGPESQIRYSMVSVPTVTSYISLEVNALVFLGKPIILPTDAT 240  
QY 241 PFVLPVRHVGTEGSMATVGLSQQLFDSALLLQKAGALNLDITGQLRSDNLLNTSALGRL 300  
Db 241 PFVLPVRHVGTEGSMATVGLSQQLFDSALLLQKAGALNLDITGQLRSDNLLNTSALGRL 300  
QY 301 IPEVARQFPPEMPVVLKVRIGATPVAMLHTNNATRLQPPFVEVLATASNSAFQSLFSLDV 360  
Db 301 IPEVARQFPPEMPVVLKVRIGATPVAMLHTNNATRLQPPFVEVLATASNSAFQSLFSLDV 360  
QY 361 VVNLRLQLSVSKVKLQGTTSVLGSDVQLTVASSNVGFDTDQVRLMGTVFEKPLLDHNA 420  
Db 361 VVNLRLQLSVSKVKLQGTTSVLGSDVQLTVASSNVGFDTDQVRLMGTVFEKPLLDHNA 420  
QY 421 LLAMGIALPGVNLHVVAPEIFVYGVVWISSGLFYQS 458  
Db 421 LLAMGIALPGVNLHVVAPEIFVYGVVWISSGLFYQS 458

RESULT 14  
US-10-176-749-498  
; Sequence 498, Application US/10176749  
; Publication No. US20030017542A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430R1C76  
; CURRENT APPLICATION NUMBER: US/10/176,749  
; CURRENT FILING DATE: 2002-06-20  
; Prior application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 498  
; LENGTH: 458  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-176-749-498

Query Match 99.8%; Score 2260; DB 12; Length 458;  
Best Local Similarity 99.8%; Pred. No. 9.2e-209;  
Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAWASRLGLLLALLLPVVGASTPGTVVRLNKAALSVYSEIGKAPLQALQVTVPHFLDWS 60  
Db 1 MAWASRLGLLLALLLPVVGASTPGTVVRLNKAALSVYSEIGKAPLQALQVTVPHFLDWS 60  
QY 61 GEALQPTIRILNVHVRHLKFTIAGFGVRLAAANFTFKVFRAPPELELTLPVELLADT 120  
Db 61 GEALQPTIRILNVHVRHLKFTIAGFGVRLAAANFTFKVFRAPPELELTLPVELLADT 120  
QY 121 RVTQSSIRTPVWSISACSLFSGHANEDGSGNSTSHALLVLVQKHKAVLSNKLCLISNL 180  
Db 121 RVTQSSIRTPVWSISACSLFSGHANEDGSGNSTSHALLVLVQKHKAVLSNKLCLISNL 180  
QY 181 VQGVNHLGTLIGLNPVGPESQIRYSMVSVPTVTSYISLEVNALVFLGKPIILPTDAT 240  
Db 181 VQGVNHLGTLIGLNPVGPESQIRYSMVSVPTVTSYISLEVNALVFLGKPIILPTDAT 240  
QY 241 PFVLPVRHVGTEGSMATVGLSQQLFDSALLLQKAGALNLDITGQLRSDNLLNTSALGRL 300  
Db 241 PFVLPVRHVGTEGSMATVGLSQQLFDSALLLQKAGALNLDITGQLRSDNLLNTSALGRL 300  
QY 301 IPEVARQFPPEMPVVLKVRIGATPVAMLHTNNATRLQPPFVEVLATASNSAFQSLFSLDV 360

Db 181 VQGVNHLGTLIGLNPVGPESQIRYSMVSVPTVTSYISLEVNALVFLGKPIILPTDAT 240  
QY 241 PFVLPVRHVGTEGSMATVGLSQQLFDSALLLQKAGALNLDITGQLRSDNLLNTSALGRL 300  
Db 241 PFVLPVRHVGTEGSMATVGLSQQLFDSALLLQKAGALNLDITGQLRSDNLLNTSALGRL 300  
QY 301 IPEVARQFPPEMPVVLKVRIGATPVAMLHTNNATRLQPPFVEVLATASNSAFQSLFSLDV 360  
Db 301 IPEVARQFPPEMPVVLKVRIGATPVAMLHTNNATRLQPPFVEVLATASNSAFQSLFSLDV 360  
QY 361 VVNLRLQLSVSKVKLQGTTSVLGSDVQLTVASSNVGFDTDQVRLMGTVFEKPLLDHNA 420  
Db 361 VVNLRLQLSVSKVKLQGTTSVLGSDVQLTVASSNVGFDTDQVRLMGTVFEKPLLDHNA 420  
QY 421 LLAMGIALPGVNLHVVAPEIFVYGVVWISSGLFYQS 458  
Db 421 LLAMGIALPGVNLHVVAPEIFVYGVVWISSGLFYQS 458

RESULT 15  
US-10-176-914-498  
; Sequence 498, Application US/10176914  
; Publication No. US20030017543A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430R1C83  
; CURRENT APPLICATION NUMBER: US/10/176,914  
; CURRENT FILING DATE: 2002-06-20  
; Prior application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 498  
; LENGTH: 458  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-176-914-498

Query Match 99.8%; Score 2260; DB 12; Length 458;  
Best Local Similarity 99.8%; Pred. No. 9.2e-209;  
Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAWASRLGLLLALLLPVVGASTPGTVVRLNKAALSVYSEIGKAPLQALQVTVPHFLDWS 60  
Db 1 MAWASRLGLLLALLLPVVGASTPGTVVRLNKAALSVYSEIGKAPLQALQVTVPHFLDWS 60  
QY 61 GEALQPTIRILNVHVRHLKFTIAGFGVRLAAANFTFKVFRAPPELELTLPVELLADT 120  
Db 61 GEALQPTIRILNVHVRHLKFTIAGFGVRLAAANFTFKVFRAPPELELTLPVELLADT 120  
QY 121 RVTQSSIRTPVWSISACSLFSGHANEDGSGNSTSHALLVLVQKHKAVLSNKLCLISNL 180  
Db 121 RVTQSSIRTPVWSISACSLFSGHANEDGSGNSTSHALLVLVQKHKAVLSNKLCLISNL 180  
QY 181 VQGVNHLGTLIGLNPVGPESQIRYSMVSVPTVTSYISLEVNALVFLGKPIILPTDAT 240  
Db 181 VQGVNHLGTLIGLNPVGPESQIRYSMVSVPTVTSYISLEVNALVFLGKPIILPTDAT 240  
QY 241 PFVLPVRHVGTEGSMATVGLSQQLFDSALLLQKAGALNLDITGQLRSDNLLNTSALGRL 300  
Db 241 PFVLPVRHVGTEGSMATVGLSQQLFDSALLLQKAGALNLDITGQLRSDNLLNTSALGRL 300  
QY 301 IPEVARQFPPEMPVVLKVRIGATPVAMLHTNNATRLQPPFVEVLATASNSAFQSLFSLDV 360

Db	301	IPVAVQFPEPMPVVLKVRGATPVAVLHTNATLRLQPEVEVLATASGAFQSLFSLDV	360
Qy	361	VVNRLQLSVSKVQLQTTISVLGEVQVLTWASSNVGFIDTDQVETLMGTVEKPILDHNA	420
Db	361	VVNRLQLSVSKVQLQTTISVLGEVQVLTWASSNVGFIDTDQVETLMGTVEKPILDHNA	420
Qy	421	LLANGIALPQVNLHYVAPEIFVYEGYVWISSGLFYQS	458
Db	421	LLANG-ALPGVNLHYVAPEIFVYEGYVWISSGLFYQS	458

Search completed: June 29, 2004, 11:02:31  
Job time : 50 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 29, 2004, 10:55:39 ; Search time 17 Seconds  
(without alignments)  
1402.831 Million cell updates/sec

Title: US-10-069-034-28  
Perfect score: 2265  
Sequence: 1 MAWASRLGLLLALLPVVGA.....PEIFVGVVSSGLFQYS 458

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2258	99.7	458	1	BPI1_HUMAN
2	2489	95.7	462	1	BPI1_MOUSE
3	392.5	77.3	470	1	LPC4_RAT
4	386	77.0	477	1	LPC3_MOUSE
5	380	76.8	472	1	LPC3_MOUSE
6	358	75.8	575	1	LPC4_HUMAN
7	353	75.6	473	1	LPC3_RAT
8	330.5	74.6	507	1	BPL2_HUMAN
9	313.5	73.8	509	1	BPL2_MOUSE
10	306	73.5	453	1	BPL3_HUMAN
11	283	72.5	483	1	BPI_HUMAN
12	280	72.4	449	1	BPL3_MOUSE
13	259	71.4	481	1	LBP_HUMAN
14	257.5	71.4	481	1	LBP_MOUSE
15	251	71.1	482	1	LBP_RABIT
16	250	71.0	445	1	BPI_MOUSE
17	247.5	70.9	482	1	BPI_BOVIN
18	246.5	70.9	481	1	LBP_RAT
19	173	7.6	493	1	PLTP_MOUSE
20	159.5	7.0	493	1	PLTP_HUMAN
21	138.5	6.1	473	1	LPC1_BOVIN
22	131.5	5.8	428	1	LPC1_MOUSE
23	118.5	5.2	484	1	LPC1_HUMAN
24	112.5	5.0	2432	1	Y43R_IRV6
25	109	4.8	493	1	CETP_MACFA
26	103.5	4.6	581	1	LR15_HUMAN
27	103	4.5	488	1	YAL5_HAEN
28	102.5	4.5	1118	1	CARB_YEAST
29	101.5	4.5	637	1	NUSM_STRPJ
30	100	4.4	1774	1	MSAS_PENPA
31	99.5	4.4	2067	1	NC06_MOUSE
32	99	4.4	858	1	ATMA_ECOLI
33	99	4.4	1845	1	Z236_HUMAN

34	37.5	4.3	1181	1	ITA7_HUMAN	Q13683	homo sapien
35	97	4.3	378	1	DP3B_STRPN	O06672	streptococc
36	97	4.3	501	1	DLDH_PEA	P31023	plum sativ
37	96.5	4.3	378	1	DP3B_STRRG	P59651	streptococc
38	96.5	4.3	529	1	VGJF_SVS	P04849	simian viru
39	96.5	4.3	560	1	ATP2_NICPL	P17614	nicotiana p
40	96.5	4.3	711	1	MMIA_STRCO	Q53902	streptomyc
41	96	4.2	637	1	NPT2_RAT	Q06496	rattus norv
42	96	4.2	2185	1	PKR1_DICDI	P20054	dicyostell
43	95.5	4.2	551	1	ATP2_ORYSA	Q01859	oryza sativ
44	95	4.2	394	1	LPXB_SYNY3	Q57310	synchocyst
45	95	4.2	760	1	SIX4_HUMAN	Q9ui06	homo sapien

## ALIGNMENTS

RESULT 1  
BPI1\_HUMAN  
ID BPI1\_HUMAN STANDARD; PRT; 458 AA.  
AC Q8N4F0; Q8NF07;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Bactericidal/permeability-increasing protein-like 1 precursor (Long  
DE palate, lung and nasal epithelium carcinoma associated protein 2)  
DE (RYSR)  
DE (RYSR)  
GN BPI1L OR LPLUNC2 OR C20ORF184.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Trachea;  
RX MEDLINE=22172641; PubMed=12185532;  
RA Mulero J.J., Boyle B.J., Bradley S., Bright J.M., Nelken S.T.,  
RA Ho T.T., Mize N.K., Childs J.D., Ballinger D.G., Ford J.E., Rupp P.;  
ET "Three new human members of the lipid transfer/lipoplysaccharide  
ET binding protein family (LTP/LBP).";  
RL Immunogenetics 54:293-300(2002).  
[2]  
SEQUENCE FROM N.A.  
MEDLINE=21638749; PubMed=11780052;  
DE Loukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,  
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Sagguley C.L.,  
BAiley J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,  
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,  
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,  
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,  
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,  
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
RA Graffham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
RA Lehaialaho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
RA Marst V.L., Martin S.L., McConnachie L.J., McJay K., McMurray A.A.,  
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
RA Phillimore B.J.C.T., Prachalingam S.R., Plumb R.M., Ramsay H.,  
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,  
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,  
RA Swann R.N., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,  
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,  
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
RA Rogers J.;  
ET "The DNA sequence and comparative analysis of human chromosome 20.";  
RL Nature 414:865-871(2001).  
[3]  
SEQUENCE FROM N.A.

RC TISSUE=Brain, Lung, and Testis;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,  
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gutarane P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzey D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fillion J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madar A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickens M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska O., Smallos D.E.,  
 RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [4]  
 RP SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.  
 RC TISSUE=Petal brain;  
 RX MEDLINE=22721692; PubMed=12837268;  
 RA Andrault J.-B., Gallard I., Giorgi D., Rouquier S.;  
 RT "Expansion of the BPI family by duplication on human chromosome 20:  
 RT characterization of the RY gene cluster in 20q11.21 encoding olfactory  
 RT transporters/antimicrobial-like peptides.";  
 RL Genomics 82:172-184 (2003).  
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).  
 CC -!- TISSUE SPECIFICITY: Highly expressed in tonsils, especially in  
 CC hypertrophic tonsils. Detected at very low levels in fetal liver.  
 CC -!- SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP  
 CC family.  
 CC  
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 CC  
 DR EMBL; AF465765; AA473983.1; -;  
 DR EMBL; BC034415; AA434415.1; -;  
 DR EMBL; AL121756; -; NOT ANNOTATED\_CDS.  
 DR Genew; HGNC:16177; BPI.L.  
 DR InterPro; IPR001124; LBP\_BPI\_CETP.  
 DR Pfam; PF02886; LBP2\_BPI\_CETP\_C; 1.  
 DR SMART; SM00329; BS2; 1.  
 DR PROSITE; PS00400; LBP\_BPI\_CETP; FALSE\_NEG.  
 DR SIGNAL.  
 FT SIGNAL.  
 FT CHAIN 1 20 POTENTIAL.  
 FT 21 458 BACTERICIDAL/PERMEABILITY-INCREASING  
 FT PROTEIN-LIKE 1.  
 FT DOMAIN 268 271 POLY-LEU.  
 FT CARBOHYD 96 96 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT SEQUENCE 458 AA; 49130 MW; FE647A75CC2FA2A8 CRC64;  
 Query Match 99.7%; Score 2258; DB 1; Length 458;  
 Best Local Similarity 99.8%; Pred. No. 5e-154;  
 Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 XAWASLGLHLLALLLPVVGASTGTGTVRLNKAALSYVSEIGKAPLQALQVTVPHFLDWS 60  
 DB 1 MAWASLGLHLLALLLPVVGASTGTGTVRLNKAALSYVSEIGKAPLQALQVTVPHFLDWS 60  
 QY 61 GEALQPTIRILNVHVRHLKFIAGVGVRLAAANFTKVFRAPELELTLPVELLADT 120

DB 61 GEALQPTIRILNVHVRHLKFIAGVGVRLAAANFTKVFRAPELELTLPVELLADT 120  
 QY 121 RVTOSSIRTPVWSISACSLFSGHANEFDGSNSTSHALLVLVOKHKAVLSNKLCLISNKL 180  
 DB 121 RVTOSSIRTPVWSISACSLFSGHANEFDGSNSTSHALLVLVOKHKAVLSNKLCLISNKL 180  
 QY 181 VQGVNVHLGLTGLNPNVPSQIRYSVMVPTVTSVSDYISLEWNAVLFLGKPIILPTDAT 240  
 DB 181 VQGVNVHLGLTGLNPNVPSQIRYSVMVPTVTSVSDYISLEWNAVLFLGKPIILPTDAT 240  
 QY 241 PFVLPVHVGTEGSMATVGLSQQLFDSALLLQKAGALNLDITGQSRDNNLNTSALGRL 300  
 DB 241 PFVLPVHVGTEGSMATVGLSQQLFDSALLLQKAGALNLDITGQSRDNNLNTSALGRL 300  
 QY 301 IPEVARQFPPEMPVVLKVRIGATPVAMLTNNATLRLOPPFVVLATASNAFQSLFSLDV 360  
 DB 301 IPEVARQFPPEMPVVLKVRIGATPVAMLTNNATLRLOPPFVVLATASNAFQSLFSLDV 360  
 QY 361 VVNLRLQLSVSKVKLQGTTSVLGVDVLTASSNVGFTDQVPTLMCTVFEKPLLDHNA 420  
 DB 361 VVNLRLQLSVSKVKLQGTTSVLGVDVLTASSNVGFTDQVPTLMCTVFEKPLLDHNA 420  
 QY 421 LLAMGIALPGVNLHYVAPFVYEGYVVISSGLFYQS 458  
 DB 421 LLAMGIALPGVNLHYVAPFVYEGYVVISSGLFYQS 458  
 RESULT 2  
 BPI.L MOUSE STANDARD; PRT; 462 AA.  
 ID BPI.L MOUSE AC Q8C1E1; Q8BVZ0; Q8C1E2; Q9D713; Q9D744;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Bactericidal/permeability-increasing protein-like 1 precursor.  
 GN BPI.L.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Tongue;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojohori T.,  
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawai J., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Konegaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo L.G., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilming L.G., Wyszewski-Boris A., Yanagisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki K., Shibata K., Shinagawa A.,  
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";



RL Nature 420:563-573 (2002).  
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).  
 CC -1- SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP  
 CC family.  
 CC  
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 CC  
 CC EMBL: AK03619; BAC26395.1; -  
 CC EMBL: AK03754; BAC26479.1; -  
 CC EMBL: AK028156; BAC25783.1; -  
 CC EMBL: AK028158; BAC25784.1; -  
 CC EMBL: AK075874; BAC36021.1; -  
 CC MGD; MGI:1913807; 2310034L2Rik.  
 CC InterPro: IPR001124; LBP\_BPI\_CETP.  
 CC Pfam: PF02886; LBP\_BPI\_CETP\_C; 1.  
 CC SMART; SM00329; BPI2; 1.  
 CC PROSITE; PS00400; LBP\_BPI\_CETP; FALSE\_NEG.  
 CC Signal.  
 CC SIGNAL 1 22 POTENTIAL.  
 CC CHAIN 23 462 BACTERICIDAL/PERMEABILITY-INCREASING  
 CC FT PROTEIN-LIKE 1.  
 CC FT N-LINKED (GLNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 99 99 N-LINKED (GLNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 297 297 N-LINKED (GLNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 336 336 N-LINKED (GLNAC. . .) (POTENTIAL).  
 CC FT CONFLICT 73 73 Q -> H (IN REF. 1; BAC25783).  
 CC FT CONFLICT 108 108 P -> T (IN REF. 1; BAC25783).  
 CC FT CONFLICT 134 134 I -> A (IN REF. 1; BAC25783).  
 CC FT CONFLICT 143 143 P -> L (IN REF. 1; BAC26479).  
 CC FT CONFLICT 251 251 P -> L (IN REF. 1; BAC26395).  
 CC FT CONFLICT 422 422 T -> P (IN REF. 1; BAC36021).  
 CC FT CONFLICT 419 419 L -> V (IN REF. 1; BAC36021).  
 CC SEQUENCE 462 AA; 49521 MW; 5D4F6D1F2AD57F45 CRC64;  
 CC  
 CC Query Match 65.7%; Score 1489; DB 1; Length 462;  
 CC Best Local Similarity 67.9%; Pred. No. 4.4e-99;  
 CC Matches 313; Conservative 49; Mismatches 95; Indels 4; Gaps 2;  
 CC  
 CC 1 MWASRLGILLALL---PVGASTPGTVVRLKKAALSYSVSIKAPLQALQVTPHPL 57  
 CC 1 MARACSLGLLLLLLRVTVTSLPVIIVRLKKAALDVSIGKAPLQALQVTSDFM 60  
 CC  
 CC 58 DWSGEALOPTRIRILNVHPRHLKFIAGFGVRLAALAAFTKVFRAPELELTLPVELL 117  
 CC 61 DPSGEVLOSTRVQILDAHVFFYLLKFIAGFGVHLSAAANFTIKVSPPEMELVLPDIL 120  
 CC  
 CC 118 ADTRVTSQSIPTPVVSIACSLFSGEANEFDGNSNSTSHALLVLVQKHKAVLSNKLCLSI 177  
 CC 121 ADVHVARDISGTVLVSFACSSIFSPAGMLDGSISTQELLDVQVHEHIKADLNKLCHV 180  
 CC  
 CC 178 SNLVGVNVHGLTGLINMPVGPESQIRYSMVSVPTVSDYISLEVNALFLGKPIILPT 237  
 CC 181 YGLVQDLNVHGLTGLISLVGPESQIRYSITSMPTITSNYISLDIGAILSLGLKPIILPM 240  
 CC  
 CC 238 -DATEPFLVPRHVTGEGSMATVGLSLOOLPDSALLLOKAGALNLDITGQSRDNLNTSA 296  
 CC 241 HGAHFVLPWPLGDAGAVTGLSLOLFEDCA-LMLQKAGSLNLEITGQINSKKNPLNTSV 300  
 CC  
 CC 297 LGRLLPEVAROPPEPMPVVLKVLGATPVAMHTNNATLRLOPFVEVLATANSFQSLF 356  
 CC 301 LGQLIPEVAHLFPEPTPLVLKVLGATPVLTHTSNSTLQQLPVEVFAAPSNAALQELF 360  
 CC  
 CC 357 SLDVVNVRLQLSVSKVLQGTTSVLGQVLTAVSSNVGFIDTDQVRLTGMGVPEKPLLD 416  
 CC 361 SLDVVNVNLDQLSVSKAKLRGTSLSLGGFQLSVATNSVNGSVDMQVLTITSTVFQKPLD 420  
 CC  
 CC 417 HLNALLAMGIALPGVNVNLAHYAPLFFVYEGYVYVSSGLFYQ 457

Db 421 HLNALLGQGVVLPRVNLHYHSEVLVREGYVVVSSGLAYQ 461

# RESULT 3

ID LPC4 RAT STANDARD; PRT; 470 AA.  
 AC Q05704;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Long palate, lung and nasal epithelium carcinoma associated protein 4  
 DE (Potential ligand-binding protein RY2G5) (Fragment).  
 GN LPLUNC4 OR RY2G5.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Fischer; TISSUE=Olfactory epithelium;  
 RX MEDLINE=92007724; PubMed=1915264;  
 RA Dear T.N., Boehm T., Reverne E.B., Rabbitts T.H.;  
 RT "Novel genes for potential ligand-binding proteins in subregions of  
 RT the olfactory mucosa";  
 RL EMBL J. 10:2813-2819 (1991).  
 CC -1- FUNCTION: May have the capacity of recognizing and binding  
 CC specific classes of odorants, may act as carrier molecules,  
 CC transporting odorants across the mucus layer to access the  
 CC receptor sites. May serve as a primary defense mechanism by  
 CC recognizing and removing potentially harmful odorants or  
 CC pathogenic microorganisms from the mucosa or clearing the excess  
 CC odorant from the mucus to enable new odorant stimuli to be  
 CC received. May bind polychlorinated biphenyls thereby protecting  
 CC lung epithelial cells from damage by such molecules.  
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).  
 CC -1- TISSUE SPECIFICITY: Highly expressed in olfactory mucosa but  
 CC undetectable in thymus, kidney, lung, brain, spleen and liver.  
 CC -1- SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP  
 CC family.

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EMBL: X60660; CAA43067.1; -  
 InterPro: IPR001124; LBP\_BPI\_CETP.  
 Pfam: PF02886; LBP\_BPI\_CETP\_C; 1.  
 SMART; SM00328; BPI1; 1.  
 SMART; SM00329; BPI2; 1.  
 PROSITE; PS00400; LBP\_BPI\_CETP; FALSE\_NEG.  
 NON TER 1 1 GLY-RICH.  
 FT DOMAIN 10 81 N-LINKED (GLNAC. . .) (POTENTIAL).  
 FT CARBOHYD 128 128 N-LINKED (GLNAC. . .) (POTENTIAL).  
 SEQUENCE 470 AA; 49593 MW; A4DF9403166AC926 CRC64;

Query Match 17.3%; Score 392.5; DB 1; Length 470;  
 Best Local Similarity 26.9%; Pred. No. 9.6e-21;  
 Matches 109; Conservative 81; Mismatches 182; Indels 33; Gaps 5;

QY 67 TRIRILNVHPRHLKFIAGFGVRLAALAAFTKVFRAPELELTLPVELLADTRVTSQ 126  
 DB 80 TGLRIVELTFRVSVRLPGLPGVGVLSLTRYVAINGKSLTGFLDIAVEVNITAKVLTMDR 139  
 QY 127 IRTPVVSIACSLFSGH-----ANEFGNSNSTSHALLVLVQKHKAVLSNKLCLSI 176  
 DB 140 TGYPLVIERCTLLGGIKVLLRGLLELVDN-----LVNRVLNVLPDLCLPI 189  
 QY 177 ISNLVQGVNVHGLTGLINMPVGPESQIRYSMVSVPTVSDYISLEVNAL-----F 227

Db 190 VDVVLGVNLQGLVDSLVPLGLGSLVQVYTFSSPLVTGFELELMTLVGEAGGLIDY 249  
 QY 228 LLGKPIILPDTATPVLPRHVGTEGSMATVGLSQOLFDSALLQKAGALMDITGOLRS 287  
 Db 250 PLGKPMPLPQMPQLPMDGNTNSQLA---ISANFSLSSVLTMLQKQALDIDITDGMFE 306  
 QY 288 DDNLNTSALGRLLPEVARQPPMPVVLKVRIGATVAMHTNATRLQPPFVEVLATA 347  
 Db 307 DLPLATSTLIGALPKVFOQYPSERLTIQVNPPTVTTLQDKALVKVATSEVVVSQ 366  
 QY 348 SNSAFQSLFSDVVNLRLQLSVSKVQLQGTSTVGLGVQVLTVASSNGFDTDQVRLMG 407  
 Db 367 PNQVETICLIDVDTLLAFSVEGDKM-IDAKLTKTSLMRTSNVGNFDFVILEMLVE 425  
 QY 408 TVPEKPLDHLNALLAGIALPGVNLHYVAPEIFVYEGYVWISS 452  
 Db 426 KIFDLAPMPANNAIGSGVPLKILNIDFSNADIDVLEMLVST 470

RESULT 4  
 LPC3\_HUMAN STANDARD; PRT; 477 AA.  
 AC P59826;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DE 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Long palate, lung and nasal epithelium carcinoma associated protein 3  
 DE precursor (RYA3).  
 GN LPLUNC3 OR C20ORF185.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 [1]  
 SEQUENCE FROM N.A., AND SUBCELLULAR LOCATION.  
 RC MEDLINE=22721692; PubMed=12837268;  
 RA Andraut J.-B., Gaillard I., Giorgi D., Rouquier S.;  
 RT "Expansion of the BPI family by duplication on human chromosome 20:  
 RT characterization of the RY gene cluster in 20q11.21 encoding olfactory  
 RT transporters/antimicrobial-like peptides";  
 RL Genomics 82:172-184(2003).  
 [2]  
 SEQUENCE FROM N.A.  
 RP MEDLINE=21638749; PubMed=11780052;  
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,  
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,  
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,  
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,  
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
 RA Chapman J.C., Clamp M., Clark A.P., Clark L.N., Clark S.Y., Clee C.M.,  
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,  
 RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,  
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
 RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.J., Howden P.J.,  
 RA Huckle B., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor J.E.,  
 RA Leharlaitho M.H., Leverhwa M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
 RA Marsh V.L., Martin S.I., McConachie L.J., McLay K., McMurray A.A.,  
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,  
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,  
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,  
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
 RA Tracey A., Tromans A.C., Vaudin M., Wallis J.M.,  
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,  
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
 RA Rogers J.;  
 RT "The DNA sequence and comparative analysis of human chromosome 20";  
 RL Nature 414:865-871(2001).  
 RN [3]

RP TISSUE SPECIFICITY.  
 RX MEDLINE=21968577; PubMed=11971875;  
 RA Bingle C.D., Craven C.J.;  
 RT "PLUNC: A novel family of candidate host defence proteins expressed in  
 RT the upper airways and nasopharynx";  
 RL Hum. Mol. Genet. 11:937-943(2002).  
 CC -!- FUNCTION: May have the capacity of recognizing and binding  
 CC specific classes of odorants, may act as carrier molecules,  
 CC transporting odorants across the mucus layer to access the  
 CC receptor sites. May serve as a primary defense mechanism by  
 CC recognizing and removing potentially harmful odorants or  
 CC pathogenic microorganisms from the mucosa or clearing the excess  
 CC odorant from the mucus to enable new odorant stimuli to be  
 CC received (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity). Cytoplasmic  
 CC according to Ref.1.  
 CC -!- TISSUE SPECIFICITY: Detected in nasal septal epithelium.  
 CC -!- SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP  
 CC family.  
 CC -!- CAUTION: Ref.2 sequence differs from that shown due to erroneous  
 CC gene model prediction.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 DR EMBL; AF549189; AAP84989.1;  
 DR EMBL; AL121756; CAC18886.1; ALT\_SEQ.  
 DR Genbank; HGNC:16178; C20orf185.  
 DR InterPro; IPR001124; LBP\_BPI\_CETP.  
 DR Pfam; PF02886; LBP\_BPI\_CETP\_C; 1.  
 DR SMART; SM00328; BPI1; 1.  
 DR SMART; SM00329; BPI2; 1.  
 DR PROSITE; PS00490; LBP\_BPI\_CETP; FALSE\_NEG.  
 KW SIGNAL.  
 FT CHAIN 1 20 POTENTIAL.  
 FT 21 477 LONG PALATE, LUNG AND NASAL EPITHELIUM  
 FT CARCINOMA ASSOCIATED PROTEIN 3.  
 FT DOMAIN 17 233  
 FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 17 17 MISSING (IN REF.1).  
 SQ SEQUENCE 477 AA; 50505 MW; 00C83FDF468BB9F6 CRC64;  
 Query Match 17.0%; Score 386; DB 1; Length 477;  
 Best Local Similarity 28.3%; Pred. No. 2.9e-20;  
 Matches 136; Conservative 90; Mismatches 207; Indels 48; Gaps 13;  
 QY 9 LVAL--LPLVVGASTP-----GTVRLNKAALSYV---SEIGKAPLQAL-QVT- 52  
 Db 4 VMLALWSLLMLGLATPYCOELLETVGLTARIDKDELGAIQNSLVEPIQLVGLSVTA 63  
 QY 53 VPHELDWSGEAL-----OPTIRILNVHVRHLKFIAGGVRLIAAAN 96  
 Db 64 VNRGLSGGLGGGLLGHGGVGVVEELSGUKHEELTPKVLKLLPFGVQL----S 119  
 QY 97 FTFKV-FRAPEP-----LELTPVELLADTRVTCSSIRTPVWSISACSLFSGHANEFDSGN 151  
 Db 120 LHTKVMGHCSPGLGLQLQLAARVNTSRVALAVSSRGTPILILKRCSTLGLHSLPSGLL 179  
 QY 152 STSHALLVLVQKHIAVLSNKLCLISNLVQGVNVHLGTLIGNVPVGPESQIRYSMVSP 211  
 Db 180 PT--PLFGVVEQMLPKVLPGLLCPVVDVSLGVVNEELGAVLGLVSLGALGVSVEFSLATLP 237  
 QY 212 TVTSDYISLVNNAVL--FLILGKPIILPTDTPVLRHVGTEGSMATVGLSQOLFDSALL 270  
 Db 238 LISNQYIELDINPIVKSVAAGDIIDPFKSRAPAKVP---PKDHTSQVWVPLFNTFTGL 294

271 LKAGALNDITQRLSDNDLNTSALGRLEFVARQPEPMPVVLKVLGATPVMMLHT 330  
 295 LQINGALDMDITPELVSDPLTTLAALLPEALGKPLHQQLLEFLRVREAPTTLHN 354  
 331 NNATLRLQPEVEVLATASAFSLSDVVMRLQLSVKVLQGTTSVLGDVQLTVA 390  
 355 KQALVSLPANIHLVFPVKGTPELSFELNSWTVRAQLAPSAKTLHLSLS-LERLSVKVA 413  
 391 SSMVGFDITDQVRLMGTVEKPLLDHALLAMGLALPGVNLHYVAPELFFVEGVYVI 450  
 414 SSTHAFDGRLEBWLSHVGVAYAPKLNVALDVGILPKVGNFNSVLEIVENAVL 473  
 451 S 451  
 474 T 474

## RESULT 5

LPC3\_MOUSE STANDARD; PRT; 472 AA.  
 AC Q80ZU7;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Long palate, lung and nasal epithelium carcinoma associated protein 3 precursor.  
 GN LPLUNC3.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]

SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Olfactory epithelium;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feilgold E.A., Grouse L.H., Derge J.G.,  
 Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,  
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 Stapleton M., Soares V.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
 Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mallahy S.J.,  
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 Fahey J., Helton B., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.X.,  
 Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
 Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences."

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 CC -!- FUNCTION: May have the capacity of recognizing and binding  
 CC specific classes of odorants, may act as carrier molecules,  
 CC transporting odorants across the mucus layer to access the  
 CC receptor sites. May serve as a primary defense mechanism by  
 CC recognizing and removing potentially harmful odorants or  
 CC pathogenic microorganisms from the mucosa or clearing the excess  
 CC odorant from the mucus to enable new odorant stimuli to be  
 CC received (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).  
 CC -!- SIMILARITY: Belongs to the BPI/LBP/Piunc superfamily. BPI/LBP  
 CC family.

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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).

CC EMBL; BC048084; AAH48084.1; -  
 CC InterPro; IPR001124; LBP\_BPI\_CETP.  
 CC Pfam; PF02886; LBP\_BPI\_CETP\_C; 1.  
 CC SMART; SM00328; BPI1; 1.  
 CC SMART; SM00329; BPI2; 1.  
 CC PROSITE; PS00400; LBP\_BPI\_CETP; FALSE\_NEG.  
 KW SIGNAL.  
 FT SIGNAL. 1 19 POTENTIAL.  
 FT CHAIN 20 472 LONG PALATE, LUNG AND NASAL EPITHELIUM  
 FT CARCINOMA ASSOCIATED PROTEIN 3.  
 FT DOMAIN 20 233 LEU/GLY-RICH.  
 FT CARBOHYD 138 138 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 472 AA; E80E787B8EBD4876 CRC64;

Query Match 16.8%; Score 380; DB 1; Length 472;  
 Best Local Similarity 26.3%; Pred. No. 7.6e-20;  
 Matches 126; Conservative 91; Mismatches 208; Indels 54; Gaps 13;

QY 9 LLLALLPVVG-ASTPTGTVRLNKAALSYVSEIGKA-----PLQALQVTVPH--- 55  
 DB 9 LMGLATPCIGLEETVGTTLARIDK-----DELGKATQNSLVGPIQLQNLVGTVTVNQ 62  
 QY 56 -----FLDWG-----EALQPTIRILNVHVRHLKFIAGFGVRLAAANFT 98  
 DB 63 LLGAGLGGGGLLSYGGIFSLVEELSGLKIELT--LPKVSUKLPGVGVL---NLH 116  
 QY 99 EKV-FRAPEP-----LELTLPVELLADTRVTQSSIRTPVVSISACLSFSGHANEDGSNST 153  
 DB 117 TKVSLHSGPLVGLLQAAEVNVSSKVALGMSPRGTFILVKRCSTLGHISLMSGLLPT 176  
 QY 154 SHALLVIVQKHIAVLNKLCLISNLVQGVNHLGTLIGLNPVGPESQIRYSVMVPTV 213  
 DB 177 --PIGLVEQTLCKVLPGLCPVVDVSVLWNEELGATLSLVLPLGLSGVEFTTLATPLI 234  
 QY 214 TSDYISLEVNVL-FLIGKPIILPTDATPVLPRHVGTGSMATVGLSQQLFDSALLLIQ 272  
 DB 235 SNQYIELDINPIKYSIAGVIDFPRIPKVP2---PKEDHTSQVTVPLFLFSVFGLLQ 291  
 QY 273 KAGALMDITQRLSDNDLNTSALGRLEFVARQPEPMPVVLKVLGATPVMMLHTNN 332  
 DB 292 TNGALDLDITPEVPRNVPLTTTDLAALAPALGKLPAPQHLHLSLRVTKSPVLLQNKX 351  
 QY 333 ATLRLOPFVEVLATASAFSLSDVVMRLQLSVKVLQGTTSVLGDVQLTVASS 392  
 DB 352 ATVSIPVTHVLSVSPQGTPEVALFQLNGVNTENAHLPASTKHLHLSL-LERLSVQLASS 410  
 QY 393 NVGFDITDQVRLMGTVEKPLLDHALLAMGLALPGVNLHYVAPELFFVEGVYVI 451  
 DB 411 FQPPFDASRLSEWLSDVVRAAYMQRLEHLEVGILPKLVNVFANSVVDIENAVL 469

## RESULT 6

LPC4\_HUMAN STANDARD; PRT; 575 AA.  
 ID LPC4\_HUMAN  
 AC P59827;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Long palate, lung and nasal epithelium carcinoma associated protein 4 (RY2G5).  
 GN LPLUNC4 OR C20ORF186.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SUBCELLULAR LOCATION.  
 RC TISSUE=Fetal brain;  
 RX MEDLINE=22721692; PubMed=12837268;  
 RA Andraut J.-B., Gaillard I., Giorgi D., Rouquier S.;  
 "Expansion of the BPI family by duplication on human chromosome 20:

RT Characterization of the RY gene cluster in 20q11.21 encoding olfactory  
 RL transporters/antimicrobial-like peptides.";  
 RN Genomics 82:172-184(2003).

RP SEQUENCE FROM N.A.

RX MEDLINE=21638749; PubMed=11780052;  
 RA Delcukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,  
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagnuley C.L.,  
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,  
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,  
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,  
 RA Clegg S., Cobley V.E., Collier R.B., Connor R.E., Corby N.R.,  
 RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,  
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
 RA Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
 RA Huckle E., Kimberley A.M., King A., Knights A., Laird G.K., Johnson D.,  
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Johnson D.,  
 RA Levasaitho M.H., Leverisha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
 RA Marsh V.L., Martin S.L., McConnachie L.J., McLeay K., McMurray A.A.,  
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,  
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,  
 RA Skuce C.D., Smith M.L., Soderlund C., Stewart C.A., Sulston J.E.,  
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
 RA Tracey A., Tromans A.C., Vaubin M., Wall M., Wallis J.M.,  
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,  
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
 RA Rogers J.,  
 RT "The DNA sequence and comparative analysis of human chromosome 20.";  
 RL Nature 414:863-871(2001).

CC -!- FUNCTION: May have the capacity of recognizing and binding  
 CC specific classes of odorants, may act as carrier molecules,  
 CC transporting odorants across the mucus layer to access the  
 CC receptor sites. May serve as a primary defense mechanism by  
 CC recognizing and removing potentially harmful odorants or  
 CC pathogenic microorganisms from the mucosa or clearing the excess  
 CC odorant from the mucus to enable new odorant stimuli to be  
 CC received (By similarity).

CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).

CC -!- SIMILARITY: Belongs to the BPI/LBP/plunc superfamily. BPI/LBP  
 CC family.

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CC EMBL; AF549190; AAP84990.1; ..

CC EMBL; AL121756; CAC18887.1; ..

CC Genew; HGNC:16179; C20orf186.

DR InterPro; IPR001124; LBP\_BPI\_CETP.

DR Pfam; PF02886; LBP\_BPI\_CETP\_C; 1.

DR SMART; SM00328; BPI1; 1.

DR SMART; SM00329; BPI2; 1.

FT DOMAIN 92 187

GLY-RICH

SEQUENCE 575 AA; 60950 MW; DAB804F446EF7707 CRC64;

Query Match 15.8%; Score 358; DB 1; Length 575;

Best Local Similarity 25.9%; Pred. No. 3.6e-18;

Matches 105; Conservative 81; Mismatches 185; Indels 34; Gaps 6;

QY 67 TRIRLVHVRHLKFTAGCGVRLARANTFKVRAPEPELETLPEVLLADRTVQSS 126

DB 186 TGLRIVELTLPVRSVRLPGVGVLSLYTRVAINGSKSLGFDIAVEYNITAKVLTWDR 245

QY 127 IRTVPVVSISACSLFSGH-----ANEFDGSNSTSHALLVLCVCKHKAVLSNKLCLS 176

DB 246 TGYPRIVIERCDTLGGIKVKLLRGLLPNLVDN-----LVNRVLADVLDELCP 295

QY 177 ISNVLQGVNVLHGLTGLNPNVGPESQIRYSMSVPTVTSDYISLEVNVL-----F 227

DB 296 VDVVLGLVNDQLGLVDSLIPGLIGSVQVTFSSLFVLTGFELELDLNTLVGRAGGLIDY 355

QY 228 LGLKPIILPTDPTFVLPVPHVGTGSMATVGLSQQLDSALLLLQKAGALNLDITQOLRS 287

DB 356 PLGWPAVSP-KMPPELPMPGMDTKSOLA---NSANFLGSLVTLLOKHALELDITNGMPE 411

QY 288 DNNLNTSALGRLEIEVARQFPEPVPVVLKVLGATPVAMLHTNNATLRLQPFVEVLATA 347

DB 412 ELPPIITATGALIEKVFQOXPESCELIIRIQVLPNPSVLMQKDKALVKVLATAEYVWSQ 471

QY 348 SNSAFQSFSLDVMNLRQLQSVSKVKLQGTTSVLGDEVLTIVASSNVGFTDITDQVRLMG 407

DB 472 PKDLTEITCLIDVDTEFLASPTEGDKLM-IDAKLEKTSINLRSTNSVGNFIDGLMEVIVE 530

QY 408 TVPEKPLDLHALLAMGIALPGVNVHLVVAPEIFVYEGYVWISS 452

DB 531 KIFDLAFWPAFMANAVLGSVPLPKILNIDFSNADIDVLEDLVLSA 575

RESULT 7

LPC3\_RAT

ID LPC3\_RAT STANDARD; PRT; 473 AA.

AC Q05701;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Long palate, lung and nasal epithelium carcinoma associated protein 3

DE precursor (potential ligand-binding protein RYA3).

GN LPLUNC3 OR RYA3.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10116;

RN [1]

SEQUENCE FROM N.A.

RC STRAIN=Fischer; TISSUE=Olfactory epithelium;

RX MEDLINE=92007724; PubMed=1915264;

RA Dear T.N., Boehm T., Keverne E.B., Rabbitts T.H.;

RT "Novel genes for potential ligand-binding proteins in subregions of  
 the olfactory mucosa.";

RL EMBO J. 10:2813-2819(1991).

CC -!- FUNCTION: May have the capacity of recognizing and binding  
 CC specific classes of odorants, may act as carrier molecules,  
 CC transporting odorants across the mucus layer to access the  
 CC receptor sites. May serve as a primary defense mechanism by  
 CC recognizing and removing potentially harmful odorants or  
 CC pathogenic microorganisms from the mucosa or clearing the excess  
 CC odorant from the mucus to enable new odorant stimuli to be  
 CC received.

CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).

CC -!- TISSUE SPECIFICITY: Highly expressed in olfactory mucosa but  
 CC undetectable in thymus, kidney, lung, brain, spleen and liver.

CC -!- SIMILARITY: Belongs to the BPI/LBP/plunc superfamily. BPI/LBP  
 CC family.

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CC EMBL; X60658; CAA43065.1; ..

DR InterPro; IPR001124; LBP\_BPI\_CETP.

DR Pfam; PF02886; LBP\_BPI\_CETP\_C; 1.

DR SMART; SM00328; BPI1; 1.

DR SMART; SM00329; BPI2; 1.

DR PROSITE; PS00400; LBP\_BPI\_CETP; FALSE\_NEG.



```

FT CARBOHYD 257 257 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 372 372 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 415 415 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 507 AA; 56469 MW; C45285C625AC08E2 CRC64;

Query Match
Best Local Similarity 14.6%; Score 330.5; DB 1; Length 507;
Matches 117; Conservative 96; Mismatches 231; Indels 33; Gaps 12;

QY 8 GLLALLPVGAST--PGTVRLNKAALSYVSEIGKAPLQAL-QVTVPHEFDWSG-EA 63
DB 11 GCFLLNLYVSSQTTPGKARITQALDYGVQAGMKVIEQMLKEKLP---DLSCSES 67
QY 64 LQPTRIRILNVH-----VRLHLKFIAGEGVRL--AAAN-----FTFKVFA 104
DB 68 LFLKVDYVYNFNSNIKISAFSEFNTSLAFVPGVGHKALNTHGTANLSTWDGSEFLFQD 127
QY 105 PBPLETLP-VELLADTRVTOSSIRTPVVSISACSLFSGHAN-EFDGNSNTH-ALLVLV 161
DB 128 TGSADLFLSGVFTGIIILTRNDFGHPTLKLDQCYAQLSHARVFSFSELVLYNSFAEPM 187
QY 162 QKHKAIVLNKCLSLSNLVQGVNHLGLTGLNVPVPSQIRYMSVPTVTSYISL 221
DB 186 EXPILKNLEMLCPHIASEVKALNANLSTLEVTIKIDNTYLLDYS--SSPEITENYLDN 247
QY 222 VNAVLFLLGKPIILTDTPFPVLRHVGTGSMATVGLSQQLFDSALLLLQKAGALNDI 281
DB 248 LKGVFYLENTLDPSPVPVFLPER---SNSKLYIGIAEYFKSAFHTAGVFNVL 304
QY 282 TQLRSDNLLNTSALGRILPEVARQFPEPMPVLKVRLGATPVAMLTNNATLRLQPFV 341
DB 305 STEEISNHFVQNSQGLNGLSRIAEIYLSQPFMRIMATEPEIINLQPGNFTLDIPASI 364
QY 342 EVLATASNSAFQSLSDVYNLRQLSVKVLQGTTSVLGDVQLTVASSNVGFDITQ 401
DB 365 MMLTPQKSTVETIIVMDPVASTSVGLVILQGLVCSLS-LNRFRLALPESNRNIEVL 423
QY 402 VRLTNGTVFKEPLDHLNALLAMGALPGVNLVHVAPEIFVYGVVWISSGLFYQS 458
DB 424 FENILSSILHFGVLPANAKLQGGFFLSNPKFLFVNSDIEVLESFLLISTDLKYET 480

RESULT 9
BPL2 MOUSE
ID BPL2 MOUSE STANDARD; PRT; 509 AA.
AC Q8C186;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Bactericidal/permeability-increasing protein-like 2 precursor.
GN BPL2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=2354683; PubMed=1246685;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Oeato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojohori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Bacalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gasterland I., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

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RA Nagashima T., Numata K., Okido T., Pavan W.J., Perlea G., Resole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reid J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kikukawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs;
RL Nature 420:563-573 (2002).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP
CC family.
CC
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CC
CC EMBL; AK028764; BAC26108.1;
DR InterPro; IPR001124; LBP_BPI_CETP.
DR Pfam; PF01273; LBP_BPI_CETP; 1.
DR Pfam; PF02886; LBP_BPI_CETP_C; 1.
DR SMART; SM00328; BPI1; 1.
DR SMART; SM00329; BPI2; 1.
DR PROSITE; PS00400; LBP_BPI_CETP; FALSE_NEG.
KW SIGNAL.
FT CHAIN 1 23 POTENTIAL.
FT CHAIN 24 509 BACTERICIDAL/PERMEABILITY-INCREASING
FT CARBOHYD 63 63 PROTEIN-LIKE 2.
FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 92 92 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 117 117 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 215 215 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 227 227 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 357 357 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 374 374 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 509 AA; 56616 MW; 07A1E2DBAA24BD9A CRC64;

Query Match
Best Local Similarity 13.8%; Score 313.5; DB 1; Length 509;
Matches 112; Conservative 98; Mismatches 231; Indels 37; Gaps 13;

QY 9 LLLALLPVGASTPGTVRLNKAALSYVSEIGKAPL-QRALQVTPHEFDWSG-EALQP 66
DB 14 LLWSLYASSQTVTGTARITQALDYGLQGMKVLQAKIIVP---DLNGSESLKF 70
QY 67 TRI-----RIINVHV-----PRHLKFIAGFVRLA-----AANFTFK--VRAPEP 107
DB 71 LKIDVYKYNFSNINAFSPNTSLAFVPGVGHKALNTHGTANLSTWNSVKAPLFRDGA 130
QY 108 LELTLP-VELLADTRVTOSSIRTPVVSISACSLFSGHAN-EFDG-----NSTHALLVL 160
DB 131 ANFLSGIYFTGIVAFTRNDFGPALELDQCHVQSHARVFSFSELVLYNSFAEPMKP 190
QY 161 VOXHKAVLSNKLCLSLSNLVQGVNHLGLTGLNVPVPSQIRYMSVPTVTSYISL 220
DB 191 ILKMLNEMW--QLCPHIAEQVFNVALEVTIKIDNTYLLDYS--SSPEITENYLDN 248
QY 221 EVNAVLF-LGKPIILTDTPFPVLRHVGTGSMATVGLSQQLFDSALLLLQKAGALND 280

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DB 249 NLKGAFFPLESLDDPPPTAPFHLPE---SRDSMLYIGISEYFFKSAFAHYVSGALGTT 305  
 QY 281 ITQCLSDNLLNTSALGRLIPEVARQFPEPMPVLKVRGATPVAMLHNNATLRLQPF 340  
 DB 306 LSTREISNYEQVQSGSVLSKIAEIVLSQFILQMMATGPPMVLQNNLSLEFPAA 365  
 QY 341 VEVLATASNGAFSLSDVWVNLRLQLSLSKVKLQGTTSVLGDVQLTVASSNGVFDITD 400  
 DB 366 VIMLTOLDNSTIOPIVSMDFVASTVGLAILQKLCISLS-LNRFLSLPENSQRDAKV 424  
 QY 401 QVTLNCTVFEKPLDLHALLAMGIALPGVNLHYVAPFIVFVEGYVWISSGLFYQS 458  
 DB 425 RFENILSLHFGVPLANTKLOQGFELPNFYNISFINSDIEVLEGYLLVSSDIAYDT 482

RESULT 10  
 BPI3 HUMAN  
 ID BPI3 HUMAN STANDARD; PRT: 453 AA.  
 AC Q8NFQ5;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Bactericidal/permeability-increasing protein-like 3 precursor.  
 GN BPI3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Tonsil;  
 RX MEDLINE=22172641; PubMed=12185532;  
 RA Mulero J.J., Boyle B.J., Bradley S., Bright J.M., Nelken S.T.,  
 RA Ho T.T., Mize N.K., Childs J.D., Ballinger J.G., Ford J.B., Rapp P.;  
 RT "Three new human members of the lipid transfer/lipoplysaccharide  
 binding protein family (LTP/LBP).";  
 RL Immunogenetics 54:293-300(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21638749; PubMed=11780052;  
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,  
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L.,  
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,  
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,  
 RA Buck L., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
 RA Clegg S., Copley V.E., Clark G., Clark L.N., Clark S.V., Clee C.M.,  
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,  
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
 RA Grahame D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
 RA Leharshaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lowell J.D.,  
 RA Marsh V.L., Martin S.B., McConachie L.J., McKay K., McKerron T.,  
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,  
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,  
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,  
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,  
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,  
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
 RA Rogers J.;  
 RT "The DNA sequence and comparative analysis of human chromosome 20.";  
 RL Nature 414:865-871(2001).  
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).  
 CC -!- TISSUE SPECIFICITY: Detected at very low levels in normal tonsils,  
 CC and at higher levels in hypertrophic tonsils.  
 CC -!- SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP  
 CC family.

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 CC -----  
 DR EMBL: AF465767; AAM73985.1; -;  
 DR EMBL: ALL21756; -; NOT ANNOTATED CDS.  
 DR Genew; HGNC:16504; BPI3.  
 DR InterPro; IPR001124; LBP BPI CETP.  
 DR Pfam; PF02886; LBP BPI CETP\_C\_1.  
 DR SMART; SM00329; BPI2; 1.  
 DR PROSITE; PS00400; LBP\_BPI\_CETP; FALSE\_NEG.  
 KW Signal.  
 FT SIGNAL 1 18 POTENTIAL.  
 FT CHAIN 19 453 BACTERICIDAL/PERMEABILITY-INCREASING  
 FT FT 19 453 PROTEIN-LIKE 3.  
 FT CARBOHYD 114 114 N-LINKED (GLCNAC. .) (POTENTIAL)  
 FT CARBOHYD 190 190 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT SEQUENCE 453 AA; 49716 MW; 19379CA22A41CESC CRC64;  
 SQ  
 Query Match 13.5%; Score 306; DB 1; Length 453;  
 Best Local Similarity 25.2%; Pred. No. 1.4e-14;  
 Matches 117; Conservative 94; Mismatches 210; Indels 44; Gaps 16;  
 QY 9 LLLALLLPVPGA-STPGTVRLNKAALSYSSIGKAPLQALQVTVPHFLD-WSGEA--- 63  
 DB 5 LCLALCSLLTGTTRADGALLRLQMDIMNQV-----QSAMDES--HILEKMAAEAGKK 54  
 QY 64 ---LQP-----TRIRLNHVHRLHKLFIAGVGRVLLAAANFTP--KVERAPELELTPV 114  
 DB 55 QPGMKIKIGITNKKVQDVLPVITLNFVPGVGIFQCVSTGTVTKGFMGN-WEIIVAG 113  
 QY 115 ELLADTRVTQ--SSIRTPVWSISACSLFSGHANEFDGNSNSTSHALLVLVQKHKA---VJ 169  
 DB 114 NITATNRLRLRDEETGLPVFKSEGEVILNVK-----TNLPSNMLPKVNVKFLDSTLHKVL 169  
 QY 170 SNKLCISNLVGVVHGLTGLIGLNPVGPESQIRYSWVSVPTSDYISLEVNVL-FL 228  
 DB 170 PGLMCPAIDAVLVVNVKNTNLSDDPMFVGQMTGVKVV-ASAPATTASYIQLDFSPVYQQQ 229  
 QY 229 LGKPIILPTDATPVLPRHVGTEGSMATVGLSQQLFDSALLLQKAGALNDIT--GQLR 286  
 DB 230 KGKTIKLADAGEALTEPE--GYAKGSSQLLPATFISAEALLQKSHVNIQDTMIGELP 287  
 QY 287 SDNLLNTSALGRLIPEVARQFPEPMPVVLKVRGATPVAMLHNNATLRLQPFVEVIAT 346  
 DB 288 PQ-----TTKTLARFIEVAVAVPKSKPLTTQIKKKPKVTKTKGSKLLHSTLEMFAA 343  
 QY 347 ASNS-AFOSLFSLDVWVNLRLQLSVKVLQGTTSVLGDVQLTVASSNGVFIQDTQVRL 405  
 DB 344 RWRKRAPMSLFLEVHFNLKQVSVHENOQKATSLDRLLSLSRKSSSISGNFNERELTGF 403  
 QY 406 MGTVEFKPLDLHALLAMGIALPGVNLHYVAPFIVFVEGYVVI 450  
 DB 404 IISYLEEAVIPVNVQVGLPDPFLAMNLYNAELDIVENALML 448

RESULT 11  
 BPI HUMAN  
 ID BPI HUMAN STANDARD; PRT: 483 AA.  
 AC E17213; Q9BYZ9; Q9H1M2; Q9H1M8; Q9H203; Q9UD65;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Bactericidal permeability-increasing protein precursor (BPI) (CAP 57).  
 GN BPI.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.



OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-64.  
 RX MEDLINE=89255455; PubMed=2722846;  
 RA Gray P.W., Flagg G., Leong S.R., Gumina R.J., Weiss J., Ooi C.E.,  
 RA Elsbach P.;  
 RT "Cloning of the cDNA of a human neutrophil bactericidal protein.  
 RT Structural and functional correlations.";  
 RL J. Biol. Chem. 264:9505-9509(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94292492; PubMed=7517398;  
 RA Lane C.G., Seilhamer J.J., McGrogan M., Ashton N., Snable J.L.,  
 RA Lane J.C., Leong S.R., Thornton M.B., Miller K.L., Scott R.W.;  
 RT "Bactericidal/permeability-increasing protein and lipopolysaccharide  
 (LPS)-binding protein. LPS binding properties and effects on LPS-  
 mediated cell activation.";  
 RL J. Biol. Chem. 269:17411-17416(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX Xu J., Wang H.;  
 RA "Cloning of cDNA of human bactericidal/permeability-increasing  
 RT protein.";  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21638749; PubMed=11780052;  
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,  
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L.,  
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,  
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,  
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.V., Clee C.M.,  
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,  
 RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,  
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
 RA Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Hoeden J.L., Howden P.J.,  
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
 RA Lehaealaho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
 RA Marsh V.L., Martin S.L., McConachie L.J., McKay K., McMurray A.A.,  
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,  
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,  
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,  
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,  
 RA Whitbread S.J., Whittaker P., Willey D.L., Williams L., Williams S.A.,  
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
 RA Rogers J.;  
 RT "The DNA sequence and comparative analysis of human chromosome 20.";  
 RL Nature 414:865-871(2001).  
 RN [5]  
 RP SEQUENCE OF 28-42.  
 RX MEDLINE=8833057; PubMed=3667613;  
 RA Ooi C.E., Weiss J., Elsbach P., Frangione B., Mannion B.;  
 RT "A 25-kDa NH2-terminal fragment carries all the antibacterial  
 RT activities of the human neutrophil 60-kDa  
 RT bactericidal/permeability-increasing protein.";  
 RL J. Biol. Chem. 262:14891-14894(1987).  
 RN [6]  
 RP SEQUENCE OF 28-47.  
 RX MEDLINE=89315947; PubMed=2501794;  
 RA Gabay J.E., Scott R.W., Campanelli D., Griffith J., Wilde C.,  
 RA Marra M.N., Seeger M., Nathan C.F.;  
 RT "Antibiotic proteins of human polymorphonuclear leukocytes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:5610-5614(1989).  
 RN [7]  
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).  
 RX MEDLINE=97334442; PubMed=9188532;  
 RA Beamer L.J., Carroll S.F., Eisenberg D.;

RT "Crystal structure of human BPI and two bound phospholipids at 2.4-A  
 RL resolution.";  
 RL Science 276:1861-1864(1997).  
 CC -!- FUNCTION: The cytotoxic action of BPI is limited to many species  
 CC of Gram-negative bacteria; this specificity may be explained by a  
 CC strong affinity of the very basic N-terminal half for the  
 CC negatively charged lipopolysaccharides that are unique to the  
 CC Gram-negative bacterial outer envelope.  
 CC -!- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED IN POLYMORPHONUCLEAR  
 CC LEUKOCYTES (PMN) GRANULES.  
 CC -!- TISSUE SPECIFICITY: Restricted to cells of the myeloid series.  
 CC -!- DOMAIN: The N-terminal region may be exposed to the interior of  
 CC the granule, whereas the C-terminal portion may be embedded in the  
 CC membrane. During phagocytosis and degranulation, proteases may be  
 CC released and activated and cleave BPI at the junction of the N-  
 CC and C-terminal portions of the molecule, providing controlled  
 CC release of the N-terminal antibacterial fragment when bacteria are  
 CC ingested.  
 CC -!- SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP  
 CC family.  
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 CC  
 DR EMBL; J04739; AAA51841.1; ALT INIT.  
 DR EMBL; AF322588; AAG42844.1; -;  
 DR EMBL; AL359555; CAC13043.1; -;  
 DR EMBL; AL499625; CAC27350.1; -;  
 DR EMBL; AL391692; CAC10453.1; -;  
 DR PDB; 1BP1; 04-SEP-97.  
 DR PDB; 1BWF; 21-JUN-00.  
 DR Genew; HGNC:1095; BPI.  
 DR MIM; 109195; -;  
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR InterPro; IPR001124; LBP BPI CTFP.  
 DR Pfam; PF01273; LBP BPI CTFP\_1.  
 DR Pfam; PF02886; LBP BPI CTFP\_C; 1.  
 DR SMART; SM00328; BPI1; 1.  
 DR SMART; SM00329; BPI2; 1.  
 DR PROSITE; PS00400; LBP BPI CTFP; 1.  
 KW Antibiotic; Signal; Transmembrane; Glycoprotein; 3D-structure.  
 FT SIGNAL 1 27  
 FT CHAIN 28 483 BACTERICIDAL PERMEABILITY-INCREASING  
 FT PROTEIN.  
 FT SITE 236 241  
 FT TRANSMEM 365 385  
 FT CONFLICT 12 12 V -> A (IN REF. 3 AND 4).  
 FT CONFLICT 212 212 K -> E (IN REF. 4).  
 FT CONFLICT 351 351 P -> S (IN REF. 3).  
 FT CONFLICT 371 371 F -> L (IN REF. 2).  
 FT CONFLICT 400 400 N -> D (IN REF. 3).  
 FT CONFLICT 407 407 K -> R (IN REF. 3).  
 FT STRAND 32 37  
 FT HELIX 58 56  
 FT TURN 57 58  
 FT STRAND 64 70  
 FT TURN 71 73  
 FT STRAND 74 89  
 FT STRAND 93 98  
 FT TURN 99 101  
 FT STRAND 102 122  
 FT TURN 123 124  
 FT STRAND 125 149  
 FT TURN 150 153  
 FT STRAND 154 163  
 FT STRAND 168 172  
 FT TURN 174 175  
 FT HELIX 179 188



FT TURN 189 189  
 FT HELIX 217 217  
 FT TURN 218 218  
 FT STRAND 223 225  
 FT STRAND 230 233  
 FT STRAND 236 236  
 FT STRAND 241 242  
 FT STRAND 246 251  
 FT STRAND 254 257  
 FT STRAND 281 286  
 FT STRAND 287 299  
 FT TURN 300 301  
 FT STRAND 304 307  
 FT HELIX 309 311  
 FT STRAND 321 321  
 FT STRAND 322 325  
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 FT TURN 330 331  
 FT HELIX 332 335  
 FT STRAND 340 347  
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 FT TURN 375 376  
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 FT TURN 399 400  
 FT STRAND 401 408  
 FT STRAND 412 412  
 FT STRAND 415 418  
 FT TURN 419 420  
 FT HELIX 425 428  
 FT STRAND 429 450  
 FT STRAND 452 453  
 FT TURN 458 459  
 FT STRAND 460 470  
 FT TURN 471 472  
 FT STRAND 473 483  
 SQ SEQUENCE 483 AA; 53396 MW; AD58C92BCAD8F47C CRC64;

Query Match  
 Best Local Similarity 22.4%; Pred. No. 6.6e-13;  
 Matches 109; Conservative 104; Mismatches 229; Indels 44; Gaps 17;

QY 3 WASRLGLLALLLPVVGASTPGTGVVRLNKAALSYVSEIGKAPLQAL-QVTVPHFLD--- 58  
 DB 11 WVS-LMWLVAGTAVTAAVNPGVWVREISQKGLDYASQQTALQKELRIKIPDYSDSEK 69  
 QY 59 -----WSGALQPTRIRLNH---VPRHLKP-IAFGVRLAANFTKVFRAPE 106  
 DB 70 IKHLGKHYSFYSDIREFQLPSSQISMVYPVGLKFSISNANIKISGRKWAQKRFLKMSG 129  
 QY 107 PLELTP-VELLADTRV-TQSGIRTPVVSISACSLFSGHANEFDGNSVSHA--LLVLVQ 162  
 DB 130 NFDLSIEGMSIADLKLGNPTSGKPTICSC---SSHNSVHVHISKVGWLLQLPH 186  
 QY 163 KHKVAVLNKL----CLGISNLVQ--VNVHLGTLGLNPNVGPESQTRYSMVSVPTTSY 217  
 DB 187 KKIESALRNKMSQCEKVTNSVSKLPQYFQTLFPMTKIDSVAG-NYGLVAPPATTAT 246  
 QY 218 ISLEVNVLFLGKPIILPTDTPVLP--RHVGTEGSMATVGLSQCLPDSALLLQKAG 275  
 DB 247 LDVQMGFEYSNH-----HNPPFPAPPVMEFPAAHDMVYGLSLFYFFNTAGLVQEAG 301  
 QY 276 ALNLDTGLQ--RSDNLNLTSGALGLIPEVARQPEPMPVVLKVLRLGATPVAKLHTNNA 333  
 DB 302 VLKTLRDMNPKESKRLTKTFGTFLPEVAKKFPN---MKIQIHVSASTPPLSVQPT 358  
 QY 334 TIRLQPFVEVLATA--SNSAFOSLFSLDVWVNLRLQLSKVSKVLOGTTSVLGDVOLTVAS 391  
 DB 359 GLTFEAVDVQAFVLPNSLSLASLFLMGHTTGSMEVSAESNRVLGELK-LDRLLLELKH 417

QY 392 SNVGFDITDQVRITLMTGTVFEKPLDLHLNALLANGIALPGVWNLHVVAPEIFVYEGVVIS 451  
 DB 418 SNIGPFPVELLDIMNVIVPILVPRVNEKQKGFPLETPARVQLVNVVLPQHONFLLEG 477  
 QY 452 SGLFYQ 457  
 DB 478 ADVVIK 483

RESULT 12  
 BPL3\_MOUSE  
 ID\_BPL3\_MOUSE STANDARD; PRT; 449 AA.  
 AC Q8BU51; Q80ZU8;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Bactericidal/permeability-increasing protein-like 3 precursor.  
 GN BPL3.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Olfactory epithelium;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,  
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,  
 Butlerfield Y.S.N., Krzywinski M.I., Skalska U.,  
 Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE OF 335-449 FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Ovary;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
 Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
 Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
 Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
 Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
 Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
 Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
 Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
 Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 Sadelain A., Schneider C., Sempile C.A., Setou M., Shimada K.,  
 Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 Varadero R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
 Wilming L.G., Wyszynski B., Yanagisawa M., Yang I., Yang L.,  
 Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 Hirazawa-Kishikawa T., Kohno H., Nakamura M., Sakazume N., Sato K.,  
 Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
 Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

RA Miyazaki A., Sakai K., Sakai D., Shibata K., Shinagawa A.,  
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.,  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 60,770 full-length cDNAs.",  
 RL Nature 420:563-573(2002).  
 CC -!- SUBCELLULAR LOCATION: Secreted (by similarity).  
 CC -!- SIMILARITY: Belongs to the BPI/LBP/plunc superfamily. BPI/LBP  
 CC family.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL: AK087711; BAC39978.1; ALT\_INIT.  
 CC EXBL: BC048083; AAH48083.1; -.  
 CC InterPro: IPR001124; LBP\_BPI\_CETP.  
 CC SMART: SM00329; BPI2; 1; LBP\_CETP.  
 CC PROSITE: PS00400; LBP\_BPI\_CETP, FALSE\_NEG.  
 KW Signal.  
 FT SIGNAL 1 18 POTENTIAL.  
 FT CHAIN 19 449 BACTERICIDAL/PERMEABILITY-INCREASING  
 FT CHAIN 19 449 PROTEIN-LIKE 3.  
 FT CARBOHYD 115 115 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CONFLICT 385 386 FF -> SS (JN REF. 2).  
 FT SEQUENCE 443 AA; 48901 MW; EF4290C3C8301DD6 CRC64;  
 SQ  
 Query Match 12.4%; Score 280; DB 1; Length 449;  
 Best Local Similarity 23.9%; Pred. No. 9.9e-13;  
 Matches 111; Conservative 94; Mismatches 215; Indels 44; Gaps 15;  
 Qy 7 LGILLALLPVVGASTCTCTVVRINKAALSYSEIGKAPLQALCVTPHFID-WSGERALQ 65  
 Db 5 LSLVLCGLLAGTRAD-PGGLRLGMDINNH-----EVQSAMEES--HILEKMAEASN 54  
 Qy 66 P-----TRIRLVHVPRLHLKFIAGFVRLLAANFTF--KVRAPEPLELTLP 113  
 Db 55 PQGGKAIKGLSNMKVKDLEPVITLNFVPGVIGSQCVSTGWTGKFTGQGN-WEINVV 113  
 Qy 114 VELLADTRVTO-SRIETVWSISACS--LFSGHANEPPGSGNSTSHALLVLVQKHKAVLS 170  
 Db 114 LNIATDRLLODEBAG-EVFRSEGEVILSVKTN-----LPNNKAIKPFVDSTLRKVL 168  
 Qy 171 NKLCISINLVGVNHLGLTILGNFVGPESQIYSVMVSVPTVTSXYLSLEVNALFLL- 229  
 Db 169 GLMCPALDAVLEYVNNKKAKLTDMPVDKGTVIKATSPPTATASHIQVDFSPVWQLQE 228  
 Qy 230 GKPIILPTDTPFVLRHVGTGEGMATVGLSQQLFDSALLLQKAGALNL--DITGQLRS 287  
 Db 229 GQLIQLATDGS--LPEPPEGSANDSOLLSATFTLTAELALLQKLEVKLKDKEVGLPQ 285  
 Qy 288 DDNLNLSALGRLLPEVARQPEPMVVLKVLKATGVAMLHTNATLRLQFFVEVIATA 347  
 Db 286 ----NTRLTAGFIPQVAKTHKPKELIKKINKPKPVTKMAGKSLMLHGLSLEMAFA 340  
 Qy 348 SNSAF-QSLFSLDVVNLRLQLSYKVKLQSTTSVLGVDLTVASSNVGFDITDQVRLX 406  
 Db 341 RHGKXPSLFFLETHIGLEIHYSDQNPLQMTSMDSLSLARFPFSVGDFFHEALTFG 400  
 Qy 407 GTVPEKPLLDHNLALLAMGIALPGVNLVHYVAFIFVYGVVVI 450  
 Db 401 TDY-QKAVIPVNDVHLVGLPLDILLAINYNLAELDIVEDALVL 444  
 RESULT 13  
 ID\_LBP\_HUMAN  
 AC P18428; O43438; Q92672; Q9H403; Q9UD66;  
 DT 01-NOV-1990 (Rel. 16, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Lipopolysaccharide-binding protein precursor (LBP).  
 GN LBP.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90385281; PubMed=2402637;  
 RA Schumann R.R., Leong S.R., Flagg G.W., Gray P.W., Wright S.D.,  
 RA Mathison J.C., Tobias P.S., Ulevitch R.J.;  
 RT "Structure and function of lipopolysaccharide binding protein.";   
 RL Science 249:1429-1431(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9429492; PubMed=7517198;  
 RA Wilde C.G., Seilhamer J.J., McGrogan M., Ashton N., Snable J.L.,  
 RA Lane J.C., Leong S.R., Thornton M.B., Miller K.L., Scott R.W.;  
 RT "Bactericidal/permeability-increasing protein and lipopolysaccharide  
 (LPS)-binding protein. LPS binding properties and effects on LPS-  
 mediated cell activation.";  
 RL J. Biol. Chem. 269:17411-17416(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX Hubacek J.A., Aslanidis C., Schmitz G.;  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBAJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96110577; PubMed=9441745;  
 RA Kirschning C.J., Au-Young J., Lamping N., Reuter D., Pfeil D.,  
 RA Seilhamer J.J., Schumann R.R.;  
 RT "Similar organization of the lipopolysaccharide-binding protein (LBP)  
 and phospholipid transfer protein (PLTP) genes suggests a common gene  
 family of lipid-binding proteins.";  
 RL Genomics 46:416-425(1997).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RA Long J.Y., Liu J.Q., Xue Y.N., Wang H.X.;  
 RT "Cloning and sequencing of human lipopolysaccharide-binding protein  
 gene.";  
 RL Sheng Wu Huaxue Yu Shengwu Wuli Jinzhan 25:469-471(1998).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21638749; PubMed=11780052;  
 RA Deloukas P., Mathews L.H., Ashurst J., Burton J., Gilbert J.G.R.,  
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,  
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Brown A.J.,  
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,  
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,  
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.B., Corby N.R.,  
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn X.,  
 RA Ellington A.G., Frankland J.A., Fraser A., Frech L., Garner P.,  
 RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
 RA Lehaealaho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
 RA Marsh V.L., Martin S.L., McConachie L.J., McLeay K., McMurray A.A.,  
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsey H.,  
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,  
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,  
 RA Swann R.M., Symamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,  
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,  
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
 RA Rogers J.;  
 RT "The DNA sequence and comparative analysis of human chromosome 20.";



RC SEQUENCE FROM N.A.  
 RX STRAIN-BALB/C;  
 RX MEDLINE=97289150; PubMed=9144073;  
 RA Lengacher S., Jongeneel C.V., Le Roy D., Lee J.D., Kravchenko V.,  
 RA Ulevitch R.J., Glauser M.P., Heumann D.,  
 RA "Reactivity of murine and human recombinant LPS-binding protein (LBP)  
 RT within LPS and Gram-negative bacteria.";  
 RL J. Inflamm. 47:165-172(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22386257; PubMed=12477932;  
 RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins P.S., Wagner L., Shermen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S.S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Kuzny D.M., Sodergren E.C., Lu X., Gibbs R.A., Sanchez A.,  
 RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sarchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -!- FUNCTION: Binds to the lipid A moiety of bacterial  
 CC lipopolysaccharides (LPS) a glycolipid present in the outer  
 CC membrane of all Gram-negative bacteria. The LBP/LPS complex seems  
 CC to interact with the CD14 receptor.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP  
 CC family.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 DR EMBL; X99347; CAAG7271.1; -;  
 DR EMBL; BC004795; AAH04795.1; -;  
 DR HS99; P17213; BPI.  
 DR MG0; MG1:1098776; Lbp.  
 DR GO; GO:0001530; F:lipopolysaccharide binding; IDA.  
 DR InterPro; IPR001124; LBP\_BPI\_CETP.  
 DR Pfam; PF01273; LBP\_BPI\_CETP\_1.  
 DR Pfam; PF02886; LBP\_BPI\_CETP\_C; 1.  
 DR SMART; SM00328; BPI1; 1.  
 DR SMART; SM00329; BPI2; 1.  
 DR PROSITE; PS00400; LBP\_BPI\_CETP; 1.  
 KM Lipid transport; Antibiotic; Transmembrane; Glycoprotein; Signal.  
 FT SIGNAL 1 24  
 FT CHAIN 25 481  
 FT CARCXYD 300 300  
 FT CARCXYD 355 355  
 FT CONFLICT 25 25  
 FT CONFLICT 51 51  
 FT CONFLICT 102 102  
 FT CONFLICT 122 122  
 FT CONFLICT 280 280  
 FT CONFLICT 310 310  
 FT CONFLICT 313 313  
 FT CONFLICT 341 341  
 FT CONFLICT 342 342  
 FT CONFLICT 395 395  
 FT CONFLICT 418 418

SQ SEQUENCE 481 AA; 53312 MW; 34EA9C06G9AB678 CRC64;  
 Query March 11.4%; Score 257.5; DB 1; Length 481;  
 Best Local Similarity 24.7%; Pred. No. 4.4e-11;  
 Matches 121; Conservative 78; Mismatches 212; Indels 79; Gaps 21;  
 QY 7 IGLLALLPVVGASTPTGVRLNKAALSYSEIKAPLORAL-OVTPHFELDWGSE--- 62  
 DB LGLLP-LSIQGTGCWNPQWARIITDKGLAYAKAEGVALKRELYKITLP---DFSGDFKI 68  
 QY 63 -----ALQPTRIILNVHVPRLHLKFTIAGVRLAA-----ANFTKVFAPRPPLE-- 109  
 DB 69 KAVRGQYEFHSLEIQNCELRGSSSLKLLPGQGLRLAISDSSIGVGKKVKRKSFLKLHGS 128  
 QY 110 -----LTLPEVLLADTRVTQSSIRTPWVSISACSL-----FSGHA-----NEFDGS 150  
 DB 129 FDLVKGVTISVDLL-----LGMDFSGRTVSASGSSRICDLVDHISGVNGVLLNLFHQ 184  
 QY 151 NSTSHALLVVKQHKIKAVLSNKLCLSI-SNLVQGVNVHGLTILGNLPVGPESQ-----TRY 205  
 DB 185 -----IESKLQKVLKNKVCMEIQSVTSIDLPYLQTL-----PVTAEIDNVLGIDY 230  
 QY 206 SMVSVPVTSDYISLEVNVAFLILG--KPIILPTDTPFVLPRLHVTGSGMATVGLSOOL 263  
 DB 231 SLVAAPQAKAQLVDVDFKGEIFNRRHSPVATPTT--MSLPE---DSKQMYFAISDHA 285  
 QY 264 FDSALLLQKAGALNDITGQLRSDDN--LNTSALGRILPEVARQFPPEPMEVILKVRIG 321  
 DB 286 ENIASRVVHQAGYLNFSITDMLPHDSGIRLNTKAFRPTTQIYKKYKPKMLLELLRTVVS 345  
 QY 322 ATFEVAMLTNNATLRLQPFVEVLATASASQSLSDVNVNLRLOLSVSKVLOGTTTSV 381  
 DB 346 A-PILNVSPGNLSLAPQMEIEGFVILPTSAPEVFLSVNVNVEASLTNTKRTKVTGMLHP 404  
 QY 382 LGDVQLTVASSNVGFDIDQVRLTGMVTFEKLDELHALLAMG--IALPGVVNHLHYAP 439  
 DB 405 -DKAQVRLESKVGIFNVNLFQAFNLNYLLNSLYPDVNAELAQGFPLPLPRHQLHDLDF 463  
 QY 440 EI---FVYEG 446  
 DB 464 QIRKDFLYIG 473  
 RESULT 15  
 LBP\_RABIT  
 ID LBP\_RABIT STANDARD; PRT; 482 AA.  
 AC P17454;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Lipopolysaccharide-binding protein precursor (LBP).  
 GN LBP.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90385281; PubMed=2402637;  
 RA Schumann R.R., Leong S.R., Flagg G.W., Gray P.W., Wright S.D.,  
 RA Mathison J.C., Tobias P.S., Ulevitch R.J.,  
 RT "Structure and function of lipopolysaccharide binding protein.";  
 RL Science 249:1429-1431(1990).  
 RN [2]  
 RC SEQUENCE OF 27-66.  
 RC TISSUE-Serum;  
 RX MEDLINE=86306528; PubMed=2427635;  
 RA Tobias P.S., Soldau K., Ulevitch R.J.;  
 RT "Isolation of a lipopolysaccharide-binding acute phase reactant from  
 RT rabbit serum.";  
 RL J. Exp. Med. 164:777-793(1986).  
 CC -!- FUNCTION: Binds to the lipid A moiety of bacterial  
 CC lipopolysaccharides (LPS), a glycolipid present in the outer

